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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:43 ; Search time 49.0695 Seconds
(without alignments)
3447.516 Million cell updates/sec

Title: US-09-437-450A-14
Perfect score: 238
Sequence: 1 tttttttttttttggggag.....tttccgcgcgaaaaaa 238

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2.6/prodata/1/ina/5A COMB.seq.*
2: /cgn2.6/prodata/1/ina/5B COMB.seq.*
3: /cgn2.6/prodata/1/ina/6A COMB.seq.*
4: /cgn2.6/prodata/1/ina/6B COMB.seq.*
5: /cgn2.6/prodata/1/ina/PCUS COMB.seq.*
6: /cgn2.6/prodata/1/ina/backfiles1.seq.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	34	14.3	1605	4	US-09-248-796A-978
C 2	33.4	14.0	1208	3	US-09-461-474-11
C 3	31.8	13.4	1464	1	US-08-292-688A-9
C 4	31.8	13.4	1546	1	US-08-292-688A-11
C 5	31.8	13.4	1616	1	US-08-292-688A-12
C 6	31.8	13.4	1621	1	US-08-292-688A-10
C 7	31.8	13.4	1693	1	US-08-292-688A-13
C 8	31.8	13.4	1693	1	US-08-292-688A-14
C 9	31.8	13.4	3653	3	US-08-973-334-1
C 10	31.8	13.4	3653	3	US-09-563-869A-1
C 11	31.8	13.4	3653	3	US-08-549-489-1
C 12	31.8	13.4	7311	4	US-09-645-004-3
C 13	31.8	13.4	7885	4	US-09-645-004-4
C 14	31.8	13.4	9274	4	US-09-811-115-1
C 15	31.4	13.2	738	4	US-09-552-225A-10
C 16	31.4	13.2	957	4	US-10-012-605C-7
C 17	31.2	13.1	342	4	US-09-270-767-3861
C 18	31.2	13.1	342	4	US-09-270-767-19143
C 19	31.2	13.1	459	4	US-09-270-767-9771
C 20	31.2	13.1	459	4	US-09-270-767-25053
C 21	31	13.0	2115	4	US-09-614-221A-481
C 22	30.8	12.9	1724	3	US-09-197-679A-1
C 23	30.8	12.9	2244	4	US-09-601-198-149
C 24	30.6	12.9	5761	4	US-09-799-451-23
C 25	30.4	12.8	477	4	US-09-107-532A-3599
C 26	30.2	12.7	640681	4	US-09-790-988-1
C 27	30	12.6	9018	4	US-10-220-587-3

28	29.6	12.4	882	4	US-09-248-796A-131	Sequence 131, App
C 29	29.4	12.4	477	1	US-08-313-608B-2	Sequence 2, Appli
C 30	29.4	12.4	477	2	US-08-459-324-2	Sequence 2, Appli
C 31	29.4	12.4	479	1	US-08-313-608B-1	Sequence 1, Appli
C 32	29.4	12.4	479	2	US-08-459-324-1	Sequence 1, Appli
C 33	29.4	12.4	1269	4	US-09-322-409-99	Sequence 99, Appl
C 34	29.4	12.4	1269	4	US-09-322-409-101	Sequence 101, App
C 35	29.4	12.4	1269	4	US-09-451-527-99	Sequence 99, Appl
C 36	29.4	12.4	1269	4	US-09-451-527-101	Sequence 101, App
C 37	29.4	12.4	1302	4	US-09-322-409-91	Sequence 91, Appl
C 38	29.4	12.4	1302	4	US-09-322-409-93	Sequence 93, Appl
C 39	29.4	12.4	1302	4	US-09-451-527-91	Sequence 91, Appl
C 40	29.4	12.4	1302	4	US-09-451-527-93	Sequence 93, Appl
C 41	29.4	12.4	5183	2	US-08-870-518-7	Sequence 7, Appli
C 42	29.2	12.3	2604	4	US-10-101-464A-834	Sequence 834, App
C 43	29.2	12.3	18613	4	US-08-956-171E-112	Sequence 112, App
C 44	29.2	12.3	18613	4	US-08-781-986A-112	Sequence 112, App
C 45	29	12.2	180	4	US-09-513-999C-29322	Sequence 29322, A

ALIGNMENTS

RESULT 1
US-09-248-796A-978/c
; Sequence 978, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 978
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-978

Query Match	14.3%;	Score 34;	DB 4;	Length 1605;
Best Local Similarity	53.8%;	Pred. No. 0.48;		
Matches	70;	Conservative	0;	Mismatches 60; Indels 0; Gaps 0;
QY	77	ATTCCGCAATCACATTTCGGATGTTCTCGAAAGAGACTTCCCAAAGTTATTTGGAGTACTG	136	
Db	1424	AATCTTAAACAAAATTTTCGTAGATCTTGTAAAGAAATCAAAAATTTTCATCAATGTAT	1365	
QY	137	TGAAAGATTCGTCATGAAGTTTACCAAGAGCTTACTATGTGAATTAATGTCAAA	196	
Db	1364	CGATACATTTCAATATTAAGATTTTCAGAAATATTTTAAAGATCGGAAAAATTTTGAAA	1305	
QY	197	CTAGTAGTCA	206	
Db	1304	TTTGTGTCA	1295	

RESULT 2
US-09-461-474-11/c
; Sequence 11, Application US/09461474
; Patent No. 6278042
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafaleski, Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Plant Metal Transporters
; FILE REFERENCE: BB1303 US NA
; CURRENT APPLICATION NUMBER: US/09/461,474

; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/112,562
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Glycine max
US-09-461-474-11

Query Match 14.0%; Score 33.4; DB 3; Length 1208;
Best Local Similarity 54.5%; Pred. No. 0.66;
Matches 67; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 54 CAATTGCGCACTCTATTATCATCCGCAATCACAATTCGGATGTTCTCGAAAGGAC 113
DB 864 CAACAGCCCCCTTCAAGCTTAGTACATCTATCTACGAGGTGTCTTCCATCAGGAC 805
QY 114 TTCCAAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTT 173
DB 804 TTCCAAAATGTTTCGAGCATGTTGATGGTTGTCCTCCCATACAACTACTGAAAAGATTAG 745
QY 174 ACT 176
DB 744 AGT 742

RESULT 3
US-08-292-688A-9/c
; Sequence 9, Application US/08292688A
; Patent No. 5814493
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Donald L.
; APPLICANT: FISHER, Kuhia L.
; TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,688A
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 004535-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-292-688A-9

Query Match 13.4%; Score 31.8; DB 1; Length 1464;
Best Local Similarity 49.1%; Pred. No. 2.2;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 64 CTGCTATTATCCATTCGCAATCACAATTCGGATGTTCTCGAAAGGACTTCCCAAAGT 123
DB 507 CTTTCTATTATTCATTCCTTCTGAAATTCGATTAATAAGTACTATAAGA 448
QY 124 TATTGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTTCTATGTGAA 183
DB 447 TAATGATTCAATTTCTTAAACATAGTAATAATCTACCTATTGGATTGCTTTATTGGT 388
QY 184 TTAATTTGCAAACTAGTAGTCAGATCAATAAAATTTCCGCGCGAAAAA 234
DB 387 AAAATATAATTTTGTAGCAAGCAATCTTATTCTTCTGGAAGGACAAA 337

RESULT 4
US-08-292-688A-11/c
; Sequence 11, Application US/08292688A
; Patent No. 5814493
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Donald L.
; APPLICANT: FISHER, Kuhia L.
; TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,688A
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 004535-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-292-688A-11

Query Match 13.4%; Score 31.8; DB 1; Length 1546;
Best Local Similarity 49.1%; Pred. No. 2.3;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 64 CTGCTATTATCCATTCGCAATCACAATTCGGATGTTCTCGAAAGGACTTCCCAAAGT 123
DB 507 CTTTCTATTATTCATTCCTTCTGAAATTCGATTAATAAGTACTATAAGA 448
QY 124 TATTGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTTCTATGTGAA 183
DB 447 TAATGATTCAATTTCTTAAACATAGTAATAATCTACCTATTGGATTGCTTTATTGGT 388
QY 184 TTAATTTGCAAACTAGTAGTCAGATCAATAAAATTTCCGCGCGAAAAA 234
DB 387 AAAATATAATTTTGTAGCAAGCAATCTTATTCTTCTGGAAGGACAAA 337

RESULT 5

US-08-292-688A-12/c
; Sequence 12, Application US/08292688A
; Patent No. 5814493
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Donald L.
; TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,688A
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 004535-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1616 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-292-688A-12

Query Match 13.4%; Score 31.8; DB 1; Length 1616;
Best Local Similarity 49.1%; Pred. No. 2.3;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 64 CTGCTATTATCCATTCGCAATCACATTTCCGATGTTCTCGAAAGGACTTCCCAAAGT 123
DB 507 CTTTCTATTTCTTATTTCCCATTTCTGAATTTGAGTAAATAAGTACTAAAGA 448
QY 124 TATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTAA 183
DB 447 TAATGATTCATTTCTTAACATAGTAATAATCTACCTATTGGATTGCTTATTGGT 388
QY 184 TTAATTTGCAAACTAGTACATCAATAAATTTCCGCGCAAAAAA 234
DB 387 AAAAATAATATTTTACCAAGCATTTCTTATTTCTGGAAGGACAAAA 337

RESULT 6

US-08-292-688A-10/c
; Sequence 10, Application US/08292688A
; Patent No. 5814493
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Donald L.
; APPLICANT: FISHER, Kuhia L.
; TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria

STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,688A
FILING DATE: 18-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Radio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 004535-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-292-688A-10

Query Match 13.4%; Score 31.8; DB 1; Length 1621;
Best Local Similarity 49.1%; Pred. No. 2.3;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 64 CTGCTATTATCCATTCGCAATCACATTTCCGATGTTCTCGAAAGGACTTCCCAAAGT 123
DB 507 CTTTCTATTTCTTATTTCCCATTTCTGAATTTGAGTAAATAAGTACTAAAGA 448
QY 124 TATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTAA 183
DB 447 TAATGATTCATTTCTTAACATAGTAATAATCTACCTATTGGATTGCTTATTGGT 388
QY 184 TTAATTTGCAAACTAGTACATCAATAAATTTCCGCGCAAAAAA 234
DB 387 AAAAATAATATTTTACCAAGCATTTCTTATTTCTGGAAGGACAAAA 337

RESULT 7

US-08-292-688A-13/c
; Sequence 13, Application US/08292688A
; Patent No. 5814493
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Donald L.
; APPLICANT: FISHER, Kuhia L.
; TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,688A
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.

```
;
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 004535-001
; TELECOMMUNICATION INFORMATION:
; . TELEPHONE: (703) 836-6620
; . TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; . LENGTH: 1693 base pairs
; . TYPE: nucleic acid
; . STRANDEDNESS: single
; . TOPOLOGY: linear
; . MOLECULE TYPE: DNA (genomic)
;
US-08-292-688A-13

Query Match 13.4%; Score 31.8; DB 1; Length 1693;
Best Local Similarity 49.1%; Pred. No. 2.4;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 64 CTGCTATTATCCATTCGCGCAATCACATTTCCGATGTTCTCGAAAGGACTTCCCAAGT 123
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
507 CTTTCTATTCTTATTCCTCCATTTCTAACTTCTGAAATTTGATGATAAATAGTACTAAAGA 448
QY 124 TATTGGAGTACTGTGAAAGAGTTTCGTCAATGAAGTTTACCCAAAGGACTTTTACTATGTGAA 183
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
447 TAATGATTCATTCTTTAAACATAGTAATAATCTACCTATTGGATTGGTCTTATTGGT 388
QY 184 TTAATTTGCAAACTAGTAGTAGTCAATCAATATAATTTTCGCGCGCAAAAAA 234
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
387 AAAATATATAATTTTGTAGCAAGCATTTCTTATTCTTCTGAAGGACAAAA 337

RESULT 8
US-08-292-688A-14/c
; Sequence 14, Application US/08292688A
; Patent No. 5814493
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Donald L.
; APPLICANT: FISHER, Kuhia L.
; TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,688A
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 004535-001
; TELECOMMUNICATION INFORMATION:
; . TELEPHONE: (703) 836-6620
; . TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; . LENGTH: 1693 base pairs
; . TYPE: nucleic acid
; . STRANDEDNESS: single
; . TOPOLOGY: linear
; . MOLECULE TYPE: DNA (genomic)
;
US-08-292-688A-14

Query Match 13.4%; Score 31.8; DB 1; Length 1693;
Best Local Similarity 49.1%; Pred. No. 2.4;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 64 CTGCTATTATCCATTCGCGCAATCACATTTCCGATGTTCTCGAAAGGACTTCCCAAGT 123
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
507 CTTTCTATTCTTATTCCTCCATTTCTAACTTCTGAAATTTGATGATAAATAGTACTAAAGA 448
QY 124 TATTGGAGTACTGTGAAAGAGTTTCGTCAATGAAGTTTACCCAAAGGACTTTTACTATGTGAA 183
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
447 TAATGATTCATTCTTTAAACATAGTAATAATCTACCTATTGGATTGGTCTTATTGGT 388
QY 184 TTAATTTGCAAACTAGTAGTAGTCAATCAATATAATTTTCGCGCGCAAAAAA 234
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
387 AAAATATATAATTTTGTAGCAAGCATTTCTTATTCTTCTGAAGGACAAAA 337

RESULT 9
US-08-973-334-1/c
; Sequence 1, Application US/08973334
; Patent No. 6261551
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Fisher, Krishna J.
; APPLICANT: Gao, Guang-Ping
; TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
; TITLE OF INVENTION: Associated Virus, Cell Lines, and
; TITLE OF INVENTION: Methods of Production and Use
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 No. 6261551ristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0 Version 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,334
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,014
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/549,489
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GNVEN012CIPUSA
; TELECOMMUNICATION INFORMATION:
; . TELEPHONE: (215) 540-9206
; . TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; . LENGTH: 3653 base pairs
; . TYPE: nucleic acid
; . STRANDEDNESS: double
; . TOPOLOGY: not relevant
; . MOLECULE TYPE: cDNA
; . FEATURE:
; . NAME/KEY: CDS
; . LOCATION: 1521..2405
;
US-08-973-334-1

Query Match 13.4%; Score 31.8; DB 3; Length 3653;
Best Local Similarity 49.1%; Pred. No. 3.2;
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QY 184 TTAATTTGTCAACTAGTCTAGATCAATAAATTTTCGCGCGGAAAAA 234
Db 433 AAAAATAATAATTTTAGCAAGCATCTTATTCTATTCTGGAAGGACAAA 383

RESULT 12

US-09-645-004-3/c

; Sequence 3, Application US/09645004
; Patent No. 6608238
; GENERAL INFORMATION:
; APPLICANT: Gavora, Jan S.
; APPLICANT: Falconer, Marcia M.
; APPLICANT: Nguyen, Thuy H.
; APPLICANT: Benkel, Bernhard F.
; TITLE OF INVENTION: Trans-Somatics With Gene Transfer Into Mammary Epithelial Cells
; FILE REFERENCE: GALA-06402
; CURRENT APPLICATION NUMBER: US/09/645,004
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 7311
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid pLNMx
US-09-645-004-3

Query Match 13.4%; Score 31.8; DB 4; Length 7311;
Best Local Similarity 49.1%; Pred. No. 4.2;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 64 CTGCTATTATCCATTCGCAATCACATTTCCGGATGTTCTCGAAAGGACTTCCCAAAGT 123
Db 3297 CTTTCTATTTCTATTCCTCCATTTCTAATCTCTGAAATTTAGTAAATAGTACTAAAGA 3238
QY 124 TATGGAGTACTGTGAAGAGTTCGTCAAGATTTACCAAGGACTTTACTATGTGAA 183
Db 3237 TAATGATTCTTTCTTAACATAGTAATAATCTACCTATTGGATTGCTTATTGGT 3178
QY 184 TTAATTTGTCAACTAGTCTAGATCAATAAATTTTCGCGCGGAAAAA 234
Db 3177 AAAAATAATAATTTTAGCAAGCATCTTATTCTATTCTGGAAGGACAAA 3127

RESULT 13

US-09-645-004-4/c

; Sequence 4, Application US/09645004
; Patent No. 6608238
; GENERAL INFORMATION:
; APPLICANT: Gavora, Jan S.
; APPLICANT: Falconer, Marcia M.
; APPLICANT: Nguyen, Thuy H.
; APPLICANT: Benkel, Bernhard F.
; TITLE OF INVENTION: Trans-Somatics With Gene Transfer Into Mammary Epithelial Cells
; FILE REFERENCE: GALA-06402
; CURRENT APPLICATION NUMBER: US/09/645,004
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 7885
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid pLNM12x
US-09-645-004-4

Query Match 13.4%; Score 31.8; DB 4; Length 7885;
Best Local Similarity 49.1%; Pred. No. 4.3;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 64 CTGCTATTATCCATTCGCAATCACATTTCCGGATGTTCTCGAAAGGACTTCCCAAAGT 123

Db 3297 CTTTCTATTTCTATTCCTCCATTTCTAATTTGAGTAAAAATAGTACTAAAGA 3238
QY 124 TATGGAGTACTGTGAAGAGTTCGTCAAGATTTACCAAGGACTTTACTATGTGAA 183
Db 3237 TAATGATTCTTTCTTAACATAGTAATAATCTACCTATTGGATTGCTTATTGGT 3178
QY 184 TTAATTTGTCAACTAGTCTAGTCAATCAATAAATTTTCGCGCGGAAAAA 234
Db 3177 AAAAATAATAATTTTAGCAAGCATCTTATTCTATTCTGGAAGGACAAA 3127

RESULT 14

US-09-811-115-1/c
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT-034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Query Match 13.4%; Score 31.8; DB 4; Length 9274;
Best Local Similarity 49.1%; Pred. No. 4.6;
Matches 84; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
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Db 550 CTTTCTATTTCTATTCCTCCATTTCTAATTTGAGTAAATAGTACTAAAGA 491
QY 124 TATGGAGTACTGTGAAGAGTTCGTCAAGATTTACCAAGGACTTTACTATGTGAA 183
Db 490 TAATGATTCTTTCTTAACATAGTAATAATCTACCTATTGGATTGCTTATTGGT 431
QY 184 TTAATTTGTCAACTAGTCTAGTCAATCAATAAATTTTCGCGCGGAAAAA 234
Db 430 AAAAATAATAATTTTAGCAAGCATCTTATTCTATTCTGGAAGGACAAA 380

RESULT 15

US-09-552-225A-10/c

; Sequence 10, Application US/09552225A
; Patent No. 6521233
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGY ZACRP3
; FILE REFERENCE: 99-09
; CURRENT APPLICATION NUMBER: US/09/552,225A
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,199
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:48 ; Search time 279.197 Seconds
(without alignments)
4898.046 Million cell updates/sec

Title: US-09-437-450A-14

Perfect score: 238

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Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	15.5	263	16	US-10-242-535A-49714 Sequence 49714, A
2	37	15.5	263	16	US-10-085-783A-49714 Sequence 49714, A
C 3	35.8	15.0	1510	18	US-10-739-930-3393 Sequence 3393, Ap
4	34.2	14.4	4233	16	US-10-041-018-135 Sequence 135, App
C 5	33.4	14.0	499	9	US-09-783-590-5790 Sequence 5790, Ap
C 6	33.4	14.0	621	13	US-10-027-632-221058 Sequence 221058, Ap
C 7	33.4	14.0	621	13	US-10-027-632-221059 Sequence 221059, Ap
C 8	33.4	14.0	621	15	US-10-027-632-221058 Sequence 221058, Ap
C 9	33.4	14.0	621	15	US-10-027-632-221059 Sequence 221059, Ap
10	33.4	14.0	7456	15	US-10-311-455-1903 Sequence 1903, Ap
11	33.4	14.0	7456	16	US-10-240-589C-101 Sequence 101, App
C 12	33.2	13.9	429	18	US-10-425-115-45605 Sequence 45605, A

C 13	33.2	13.9	620	16	US-10-240-425-971 Sequence 971, App
14	32.8	13.8	3423	16	US-10-398-221-3632 Sequence 3632, Ap
15	32.6	13.7	615	18	US-10-425-115-59600 Sequence 59600, A
C 16	32.6	13.7	6123	15	US-10-311-455-794 Sequence 794, App
C 17	32.4	13.6	468	16	US-10-424-599-17649 Sequence 17649, A
18	32.4	13.6	586	13	US-10-027-632-111552 Sequence 111552, A
19	32.4	13.6	586	13	US-10-027-632-111553 Sequence 111553, A
20	32.4	13.6	586	15	US-10-027-632-111552 Sequence 111552, A
21	32.4	13.6	586	15	US-10-027-632-111553 Sequence 111553, A
C 22	32.2	13.5	6134	15	US-10-311-455-1155 Sequence 1155, Ap
C 23	32	13.4	559	13	US-10-027-632-232695 Sequence 232695, A
C 24	32	13.4	559	13	US-10-027-632-232696 Sequence 232696, A
C 25	32	13.4	559	13	US-10-027-632-232697 Sequence 232697, A
C 26	32	13.4	559	15	US-10-027-632-232695 Sequence 232695, A
C 27	32	13.4	559	15	US-10-027-632-232696 Sequence 232696, A
C 28	32	13.4	559	15	US-10-027-632-232697 Sequence 232697, A
C 29	32	13.4	756	13	US-10-027-632-112791 Sequence 112791, A
C 30	32	13.4	756	15	US-10-027-632-112791 Sequence 112791, A
C 31	32	13.4	5856	15	US-10-311-455-790 Sequence 790, App
C 32	32	13.4	5856	16	US-10-257-166-70 Sequence 70, Appl
C 33	32	13.4	12601	15	US-10-311-455-2180 Sequence 2180, Ap
C 34	31.8	13.4	607	13	US-10-027-632-224261 Sequence 224261, A
C 35	31.8	13.4	607	15	US-10-027-632-224261 Sequence 224261, A
C 36	31.8	13.4	2000	9	US-09-938-842A-4562 Sequence 4562, Ap
C 37	31.8	13.4	2000	11	US-09-938-842A-4562 Sequence 4562, Ap
C 38	31.8	13.4	3653	14	US-10-155-649-1 Sequence 1, Appli
C 39	31.8	13.4	5732	9	US-09-897-006-6 Sequence 6, Appli
C 40	31.8	13.4	5732	10	US-09-897-511A-6 Sequence 6, Appli
C 41	31.8	13.4	5732	15	US-10-397-079-6 Sequence 6, Appli
C 42	31.8	13.4	5732	18	US-10-759-315-6 Sequence 6, Appli
C 43	31.8	13.4	8858	15	US-10-378-393-1 Sequence 1, Appli
C 44	31.8	13.4	9274	9	US-09-811-123-7 Sequence 7, Appli
C 45	31.8	13.4	9274	9	US-09-811-115-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-242-535A-49714
; Sequence 49714, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49714
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-49714

Query Match 15.5%; Score 37; DB 16; Length 263;
Best Local Similarity 52.2%; Pred. No. 0.87;
Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 58 TGGCAACTGCTATTTCATTCGGAATCCGGAATCCACATTCGGAATGTTCTCGAAAGACTTCC 117
Db 49 TGGTAAGATTGATTATAGTTACCTCATTTTATCTAAAGGAGTTTAAAGATTG 108

QY 118 CAAAGTTATTGGAGTACTGTGAAGAGTTCGTGATGAGTTTACCCAAAGGACTTTACTA 177
Db 109 CTTTGCCCTTGATGAATTGTAACATCATGCTCCAAGAAATATAATTCCATAATTTACTA 168
QY 178 TGTGAATTAATTTGTCAAAGTAGTAGTCAGATCAATA 214
Db 169 TAAAGAGTAAATTTTAAAGCTTTATGTGTTAAATTAACA 205

RESULT 2

US-10-085-783A-49714
; Sequence 49714, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 59994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 49714
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-49714

Query Match 15.5%; Score 37; DB 16; Length 263;

Best Local Similarity 52.2%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;
Matches 82; Conservative 0;

QY 58 TGGCACTGTCTATTATCCATTCGCAATCACATTCGGATGTTCTCGAAAGGACTTCC 117
Db 49 TGGTAAGATGATTATAGTATACCTCATTTTATCTTAATGGATTTAAGTAAGTTG 108
QY 118 CAAAGTTATTGGAGTACTGTGAAGAGTTCGTGATGAGTTTACCCAAAGGACTTTACTA 177
Db 109 CTTTGCCCTTGATGAATTGTAACATCATGCTCCAAGAAATATAATTCCATAATTTACTA 168
QY 178 TGTGAATTAATTTGTCAAAGTAGTAGTCAGATCAATA 214
Db 169 TAAAGAGTAAATTTTAAAGCTTTATGTGTTAAATTAACA 205

RESULT 3

US-10-739-930-3393/c
; Sequence 3393, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3393
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER2530_2
US-10-739-930-3393

Query Match 15.0%; Score 35.8; DB 18; Length 1510;
Best Local Similarity 59.2%; Pred. No. 4.1;

Matches 61; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 1 TTTTTTTTTTTTTTTGGGAGGAATCACGGCTTCGGATGCAACAGTCTTCTCTCAATGG 60
Db 1393 TTTTTTTTTTTTGAAGAAATAAAGCGGCTTCAGGAAGCAACTGCCATCTTCCATTATC 1334
QY 61 CAACTGCTATATATCCATTCGCAATCAACATTTCCGATGTTCT 103
Db 1333 AAACTTTCCGCTAGCATTTTATGGAATACATTAGCTATGTTTT 1291

RESULT 4

US-10-041-018-135
; Sequence 135, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 135
; LENGTH: 4233
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
US-10-041-018-135

Query Match 14.4%; Score 34.2; DB 16; Length 4233;

Best Local Similarity 54.3%; Pred. No. 19;
Matches 69; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 112 ACTTCCCAAGTTATTGGAGTACTGTGAAGAGTTCGTGATGAGTTTACCCAAAGGACT 171
Db 236 ACTTCTCAGTTTTTCATAAAGTATAGGATGGAATTTAAATTAACCTTTTAACTCAA 295
QY 172 TTACTATGCAATTAATTCGCAACTAGTAGTCAGATCAATAAAATTTTCCGCGCGAAA 231
Db 296 TAAGTAATGATTAATTCGCAATTAATAAAGAGAAATTAATTTCAAAGATGA 355
QY 232 AAAAAA 238
Db 356 AAATAA 362

RESULT 5

US-09-783-590-5790/c
; Sequence 5790, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5790
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens

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; NAME/KEY: misc feature
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; LOCATION: (497)
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; US-09-783-590-5790
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Query Match 14.0%; Score 33.4; DB 9; Length 499;
Best Local Similarity 50.3%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 68 CTATTATCCATTCGCCAATCACATTTCCGGATGTTCTCGAAAGAGACTTCCCAAAGTTATT 127
Db 281 CTACTAATACNCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 222
Qy 128 GGAGTACTGTGAAAGAGTTGTCATGAAGTTTACCCAAAGAGCTTTTACTATGTAATTA 187
Db 221 TAAGTTGTTANCAACATTTTGGTTTATTCAGAACATCTTAACAGCATGTTCTCTAA 162
Qy 188 ATTGTCAAACTAGTAGTCAGATCAATAAAT 218
Db 161 ATGTTCAAATTAAGGTAATTACATGAAT 131
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RESULT 6
US-10-027-632-221058/c
; Sequence 221058, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
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; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221058
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(621)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-221058

Query Match      14.0%; Score 33.4; DB 13; Length 621;
Best Local Similarity 52.5%; Pred. No. 15;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 100 TTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTTCGTCATGAAGTTT 159
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Db 316 TACTTGTAAAGTCCTTCAGTTAATGGGTGTTAACTGAGAGAGATATTTTAGTGACTTCT 257

QY 160 ACCCAAGGACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAAAATT 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 ATGGAATATAATTAACAATAAGAGAAATATTCTAAATCCAGGTCTGAGAGAAAGGAAAA 197

QY 220 TTCCGCGCGAAAAA 238
Db 196 AGCAACTGGAAGAAAA 178

RESULT 7
US-10-027-632-221059/c
; Sequence 221059, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221058
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(621)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-221058

Query Match      14.0%; Score 33.4; DB 13; Length 621;
Best Local Similarity 52.5%; Pred. No. 15;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 100 TTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTTCGTCATGAAGTTT 159
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Db 316 TACTTGTAAAGTCCTTCAGTTAATGGGTGTTAACTGAGAGAGATATTTTAGTGACTTCT 257

QY 160 ACCCAAGGACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAAAATT 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 ATGGAATATAATTAACAATAAGAGAAATATTCTAAATCCAGGTCTGAGAGAAAGGAAAA 197

QY 220 TTCCGCGCGAAAAA 238
Db 196 AGCAACTGGAAGAAAA 178

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US-10-027-632-221058/c
; Sequence 221058, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221058
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(621)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-221058

Query Match      14.0%; Score 33.4; DB 15; Length 621;
Best Local Similarity 52.5%; Pred. No. 15;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 100 TTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTTCGTCATGAAGTTT 159
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Db 316 TACTTGTAAAGTCCTTCAGTTAATGGGTGTTAACTGAGAGAGATATTTTAGTGACTTCT 257

QY 160 ACCCAAGGACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAAAATT 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 ATGGAATATAATTAACAATAAGAGAAATATTCTAAATCCAGGTCTGAGAGAAAGGAAAA 197

QY 220 TTCCGCGCGAAAAA 238
Db 196 AGCAACTGGAAGAAAA 178
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Matches	103;	Conservative	0;	Mismatches	116;	Indels	0;	Gaps	0;
QY	2	TTTTTTTTTTTTTTGGGAGGAAATC	CGGGTTCGGATCGCAACAGCTCTCTCTCAATTGGC	61					
Db	83	TTTTTTTTTTTTTTTATGTTTATATATTTAGTTTCGTTAGTAAGTTTAGTTAGTTT	142						
QY	62	AACGTCATATATCCATTCGCAATCACATTT	CGGATGTTCTCGAAAGGACATCCCAA	121					
Db	143	AAGAGTGATTTTAAATTTGTTATTTTTTTTATATTTTATGATTTAGTTTGTGTTAA	202						
QY	122	GTTATTCGGAGTACGTCAAGAGAGTTCGTCAAGATTTAC	CCAAAGGACATTTACTATGTG	181					
Db	203	GTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTGTTT	262						
QY	182	AATTTAAATTCGCAACTAGTAGTCAGATCAATAAAATTT	220						
Db	263	TATTTAGTAAATTTAAATTAATTTTAAAAAATAAAAAAATTT	301						

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RESULT 12
US-10-425-115-45605/c
; Sequence 45605, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 45605
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(429)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_141598C.1
; US-10-425-115-45605

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RESULT 13
US-10-240-425-971/c
; Sequence 971, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Bolland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026

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; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 971
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AI890347
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(620)
; OTHER INFORMATION: n = a o r c g o r t
US-10-240-425-971

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	Query Match	13.9%;	Score 33.2;	DB 16;	Length 520;
	Best Local Similarity	53.5%;	Pred. No. 17;		
Matches	91; Conservative	0;	Mismatches 78;	Indels 1;	Gaps 1;
QY	70	ATTATCCATTCGCAATCACATTTCGGAGTCTCTCGAAAGGACTTTCCCAAAGCTTAATGG			
Db	182	ATTTTAAAATGACCAAGAATGTGAAGTTCAGATTATCTCTTCTGATGATGTTTT			
QY	130	AGTACTGTG-AAAGAGTTCGTGCATGAAGTTTACCCAAAGGACTTTACTATGTGAATATAA			
Db	122	TTTCCTCTGTGATGAGTGTGTTCTGACTTTTTTCCCTTTTGATTCTGTAIGTGAATTAAG			
QY	189	TGTCAAACTAGTAGTCAGATCAATAAATTTTCCGCGCGAAAAAAA			
b	62	ATCTAAAAATAAAGGTGCGCTGATTATTTTTCGAAAAAAAAAAAAAAAA			

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RESULT 14
US-10-398-221-3632
; Sequence 3632, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3632
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Listeria monocytogenes 4b
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
; US-10-398-221-3632

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	Query Match	13.8%	Score 32.8;	DB 16;	Length 3423;
	Best Local Similarity	59.8%;	Pred. No. 45;		
	Matches 55;	Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;
Qy	60	GCAACTGCTATTATCCANTCCGCAATCACATTTCGGATGTTTCGAAAGGACTTCCCA	119		
Db	2377	GAATTTGTTTTTATCTTTTTCCCAAGCACAAACGAATGGTATGGATGAAACTTCGT	2436		
Ov	120	AAGTTATTCGAGTACTGTGAAAGAGTTTCGTCA	151		

Search completed: January 22, 2005, 05:10:45
Job time : 283.197 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:43 ; Search time 44.1213 Seconds
(without alignments)
3447.516 Million cell updates/sec

Title: US-09-437-450A-34

Perfect score: 214

Sequence: 1 aaatcatggcggcgatgca.....acgtggagaaaaaa 214

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTOTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	35.2	16.4	1664976	4	US-08-916-421B-1
C 2	35.2	16.4	1664976	4	US-09-692-570-1
C 3	34.8	16.3	10754	2	US-08-966-958-1
C 4	34.8	16.3	10754	2	US-09-215-817-1
C 5	34.8	16.3	10754	3	US-09-342-353-1
C 6	33.8	15.8	184	4	US-09-513-999C-28584
C 7	33.8	15.8	1113	4	US-09-647-224A-23
C 8	33.6	15.7	231	4	US-09-107-532A-2950
C 9	33.4	15.6	12173	4	US-08-956-171B-310
C 10	33.4	15.6	12173	4	US-08-781-986A-310
C 11	32.8	15.3	696	3	US-09-227-357-69
C 12	32.8	15.3	1476	4	US-09-134-000C-1200
C 13	32.6	15.2	277	4	US-09-621-976-17619
C 14	32.6	15.2	495	4	US-09-270-767-28358
C 15	32.6	15.2	979	4	US-09-270-767-12569
C 16	32.6	15.2	1551	4	US-09-270-767-29950
C 17	32.6	15.2	1599	4	US-09-270-767-13884
C 18	32.4	15.1	270	3	US-09-134-001C-1648
C 19	32.4	15.1	1269	4	US-09-322-409-99
C 20	32.4	15.1	1269	4	US-09-322-409-101
C 21	32.4	15.1	1269	4	US-09-451-527-99
C 22	32.4	15.1	1269	4	US-09-451-527-101
C 23	32.4	15.1	1302	4	US-09-322-409-91
C 24	32.4	15.1	1302	4	US-09-322-409-93
C 25	32.4	15.1	1302	4	US-09-451-527-91
C 26	32.4	15.1	1302	4	US-09-451-527-93
C 27	32.4	15.1	3204	4	US-09-710-279-3528

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C 28 32.4 15.1 3473 4 US-09-710-279-3343 Sequence 3343, Ap
C 29 32.4 15.1 3546 4 US-09-710-279-3457 Sequence 3457, Ap
C 30 32.4 15.1 8654 1 US-08-920-812-6 Sequence 6, Appli
C 31 32.4 15.1 8654 1 US-08-920-827-6 Sequence 6, Appli
C 32 32.4 15.1 8654 1 US-08-921-177-6 Sequence 6, Appli
C 33 32.4 15.1 8654 1 US-08-362-577C-6 Sequence 6, Appli
C 34 32.4 15.1 8654 2 US-08-920-828-6 Sequence 6, Appli
C 35 32.4 15.1 640881 4 US-09-790-988-1 Sequence 1, Appli
C 36 32.2 15.0 45546 3 US-09-146-053-6 Sequence 6, Appli
C 37 31.8 14.9 1092 4 US-09-328-352-3578 Sequence 3578, Ap
C 38 31.8 14.9 5152 4 US-10-204-708-74 Sequence 74, Appl
C 39 31.4 14.7 1168 4 US-08-961-527-362 Sequence 362, App
C 40 31.2 14.6 2214 4 US-10-327-189-1 Sequence 1, Appli
C 41 30.8 14.4 2595 4 US-09-919-497-12 Sequence 12, Appl
C 42 30.8 14.4 4079 4 US-09-016-434-1257 Sequence 1257, Ap
C 43 30.8 14.4 4105 3 US-08-121-446-1 Sequence 1, Appli
C 44 30.8 14.4 1664976 4 US-08-916-421B-1 Sequence 1, Appli
C 45 30.8 14.4 1664976 4 US-09-692-570-1 Sequence 1, Appli

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ALIGNMENTS

RESULT 1

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US-08-916-421B-1/C
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
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; LOCATION: (84773)..(84773)
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
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; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664855)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1
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Query Match 16.4%; Score 35.2; DB 4; Length 1664976;

Best Local Similarity 53.7%; Pred.No.5.2;

Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Db 501863 GAGGAAAAATTCCTAAAGGAGTTGGAGGAGTTTGTAAAAATCTAAAGGAGGACTAAA 501804
QY 139 AGGACTTTTACTATGTGAATTAATTTCAACTAGTAGTCAGATCAATAAATTTTACGT 198
Db 501803 AAGAAGGCTAAAGTAGTACTATAAAAAATTAACAGAAATATTCAATAAAGAAATATTTTAT 501744
QY 199 GGAATAAAAAAATAAAA 214
Db 501743 AGGACAAATAAAGTAA 501728
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RESULT 2
; US-09-692-570-1/c
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6797466
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10398)..(10398)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
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; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
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; LOCATION: (234220)..(234220)
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; LOCATION: (234814)..(234814)
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; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
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; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
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; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g

Query Match 16.4%; Score 35.2; DB 4; Length 1664976;
Best Local Similarity 53.7%; Pred. No. 5.2;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 79 GAAAGGACTTCCCAAGTTATTGGAGTACTGTGAAAGAGTTCGTATGAGTTTCCCAA 138
DB 501863 GAGGAAATTCCTTAAGAGTGTGGAGGTTTGTAAATCTAAAGGAGGACTAAA 501804

QY 139 AGGACTTTACTATGTGAATTAATTTGTCAACTAGTAGTCAGATCAATAAATTTTACGT 198
DB 501803 AAGAGGCTAAAGTAGCTATATAAATTAACAGATATTTCAATAAAGAAATATTTTAT 501744

QY 199 GGAAGAAAAA 214
DB 501743 AGGACATAAAGTAA 501728
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RESULT 3
US-08-966-958-1
; Sequence 1, Application US/08966958
; Patent No. 5928908
; GENERAL INFORMATION:
; APPLICANT: Dunn, John
; APPLICANT: Randesi, Matthew
; TITLE OF INVENTION: METHODS FOR INTRODUCING UNIDIRECTIONAL
; TITLE OF INVENTION: DELETIONS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET: P.O. Box 5000
; CITY: Upton
; STATE: New York
; COUNTRY: US
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,958
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: AUI97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 344-3341
; TELEFAX: (516) 344-3729
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-966-958-1

Query Match 16.3%; Score 34.8; DB 2; Length 10754;
Best Local Similarity 53.7%; Pred. No. 1.3;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 80 AAAGGACTTCCCAAGTTATTGGAGTACTGTGAAAGAGTTCGTATGAGTTTCCCAA 139
DB 2311 ATAGGGAATATATATCTTTATTTTGTGACAGGCAATATTTCTCTAGAGGTCACAAA 2370

QY 140 GGACTTTTACTATGTGAATTAATTTGTCAACTAGTAGTCAGATCAATAAATTTTACGTG 199
DB 2371 AGTAACTAATAAGGAAAAAATTGACAAACTGGACTTCATCAAAATTAATCATCTTTT 2430

QY 200 GAAAAA 213
DB 2431 GTTCATCAAGAAA 2444

RESULT 4
US-09-215-817-1
; Sequence 1, Application US/09215817
; Patent No. 5968786
; GENERAL INFORMATION:
; APPLICANT: Dunn, John
; APPLICANT: Randesi, Matthew
; TITLE OF INVENTION: METHODS FOR INTRODUCING UNIDIRECTIONAL
; TITLE OF INVENTION: DELETIONS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET: P.O. Box 5000
```

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; CITY: Upton
; STATE: New York
; COUNTRY: US
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,817
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/966,958
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogesian, Margaret
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: AU197-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 344-3341
; TELEFAX: (516) 344-3729
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-215-817-1

Query Match 16.3%; Score 34.8; DB 2; Length 10754;
Best Local Similarity 53.7%; Pred. No. 1.3;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 80 AAAGGACTTCCCAAGTTATTGGAGTACTGTGAAGAGTTCGTGATGAAGTTTCCCAA 139
Db 2311 ATAGGGAAATATAATCTTTATTTGTGACAGGCAAAATATTTCTCTAGAGGGTCACAAA 2370
QY 140 GGACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAATAATTTTACGTG 199
Db 2371 AGTAACTAATAGGGAAATAATTTGACAACTGGACTTCATCAAAATTAATCATCTTTT 2430
QY 200 GAAAAAATAAAAAA 213
Db 2431 GTTCATCAAGAAA 2444

RESULT 6
US-09-513-999C-25584
; Sequence 25584, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 25584
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-25584

Query Match 15.8%; Score 33.8; DB 4; Length 184;
Best Local Similarity 58.4%; Pred. No. 0.64;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 111 TGAAGAGTTGCGTCATGAAGTTTCCCAAGGACTTTTACTATGTGAATTAATTTTAAAT 170
Db 5 TAAAAAGGTAGAAAGTAATTTTCTTAAATAATAAATAAATAAATAAATAAATAAATAAATAA 64
QY 171 TAGTAGTCAGATCAATAATAATTTTACGTGCAAAAAAATAAATAAATAAATAAATAAATAA 211
Db 65 TCATAAGCACATAATAATAGAACTTTACCAGGAGAGAGAAAAA 105

RESULT 7
US-09-647-224A-23
; Sequence 23, Application US/09647224A
; Patent No. 6482631
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Guttridge, Steven
; APPLICANT: Hitz, William D.
; APPLICANT: Maxwell, Carl A.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tao, Yong
; APPLICANT: Vollmer, Steven J.
; TITLE OF INVENTION: TRYPTOPHAN BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB-1150-A
; CURRENT APPLICATION NUMBER: US/09/647,224A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/079,386
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/06046
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23

; CITY: Upton
; STATE: New York
; COUNTRY: US
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,817
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/966,958
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogesian, Margaret
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: AU197-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 344-3341
; TELEFAX: (516) 344-3729
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-215-817-1

Query Match 16.3%; Score 34.8; DB 3; Length 10754;
Best Local Similarity 53.7%; Pred. No. 1.3;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 80 AAAGGACTTCCCAAGTTATTGGAGTACTGTGAAGAGTTCGTGATGAAGTTTCCCAA 139
Db 2311 ATAGGGAAATATAATCTTTATTTGTGACAGGCAAAATATTTCTCTAGAGGGTCACAAA 2370
QY 140 GGACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAATAATTTTACGTG 199
Db 2371 AGTAACTAATAGGGAAATAATTTGACAACTGGACTTCATCAAAATTAATCATCTTTT 2430
QY 200 GAAAAAATAAAAAA 213
Db 2431 GTTCATCAAGAAA 2444

RESULT 5
US-09-342-353-1
; Sequence 1, Application US/09342353
; Patent No. 6248569
; GENERAL INFORMATION:
; APPLICANT: Dunn, John
; TITLE OF INVENTION: METHOD FOR INTRODUCING UNIDIRECTIONAL NESTED DELETIONS
; FILE REFERENCE: CIP OF U.S. Application 08/966,958
; CURRENT APPLICATION NUMBER: US/09/342,353
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 08/966,958
; EARLIER FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-353-1

Query Match 16.3%; Score 34.8; DB 3; Length 10754;
Best Local Similarity 53.7%; Pred. No. 1.3;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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US-09-107-532A-2950
Query Match      15.7%; Score 33.6; DB 4; Length 231;
Best Local Similarity 54.2%; Pred. No. 0.78;
Matches 90; Conservative 0; Mismatches 74; Indels 2; Gaps 1;

QY 1 AAATCATGGCGCGGATGCAACAGCTTCTCTCAATTTGGCAACTGTCTATATCATTTCCGCCAA 60
Db 65 AAAGCCTTAATCCGACAGCTTCTGTGTTTACCATTGGCGACTTTCGACGTTTCTCGGCCAA 124
QY 61 CACATTTCCGATGTTCTCGMAAAGGACTTCCCAAGTTATTGGAGTA--CTGTGAAAGAG 118
Db 125 CAGCCTATGTTTGTATAGAGCCTCACCTAACAGGTTATTACTATATCTATATTTACGAG 184
QY 119 TTTCGTCAATGAATTTCCCAAGGACTTTACTATGTGAATTAATG 164
Db 185 TTCAATGATAGACTTTTCTTAATGATTAGGCAATGGAATTTGAAATG 230

RESULT 9
US-08-956-171E-310
; Sequence 310, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Rannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 45,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 310:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 310:
US-08-956-171E-310
Query Match      15.6%; Score 33.4; DB 4; Length 12173;
Best Local Similarity 58.6%; Pred. No. 3.4;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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US-09-107-532A-2950
Query Match      15.8%; Score 33.8; DB 4; Length 1113;
Best Local Similarity 52.5%; Pred. No. 1.2;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 73 GTTCTCGAAAGGACTTCCCAAGTTATTGGAGTACTGTGAAAGAGTTGTCATGAGATT 132
Db 973 GGTCTCTATTAGACGCCGCCAGGCTTATTGTAGCTTCTTGTTCAGTTTGTGAAGACATT 1032
QY 133 TCCCAAGAGGACTTACTATGTGAATTAATTTGCAAACTAGTAGTCAGATCAATAAAATT 192
Db 1033 TGAATAATAGCTGCTCGAATGATAGCAGTAATAAACAACACTTTGAAGCGGAGTCCCAAC 1092
QY 193 TTACGTGGAAAAAATAAAAAA 213
Db 1093 TAAAAAATAAAAAAATAAAAAA 1113

RESULT 8
US-09-107-532A-2950
; Sequence 2950, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2950:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...231
; SEQUENCE DESCRIPTION: SEQ ID NO: 2950:
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (605)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (648)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (655)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-69

Query Match      15.3%; Score 32.8; DB 3; Length 696;
Best Local Similarity 51.4%; Pred. No. 1.9;
Matches 73; Conservative 1; Mismatches 68; Indels 0; Gaps 0;

QY 71 ATGTTCTCGAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAG 130
Db 278 ATGCTTTTAAATAATCWAACAACTAACTAATATCAGTAGCCATCGAGTCATCGGCTTGAGG 219
QY 131 TTTCCCAAAGGACTTTTACTATGTGAATTAATTTGTAATTTGTCAAAGTACTAGTCAGATCAATAAAA 190
Db 218 GTAAACTAATCCCTTATACCACTTGATTTATTATTAATTAGTTAATAATGTCAGTTAAT 159
QY 191 TTTTACGTGGAAGAAAAA 212
Db 158 TTCAACTGCAAAAGAAAAA 137

RESULT 12
US-09-134-000C-1200
; Sequence 1200, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1200
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1200

Query Match      15.3%; Score 32.8; DB 4; Length 1476;
Best Local Similarity 56.5%; Pred. No. 2.5;
Matches 61; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 94 AAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTCCCAAAGGACTTTTACTATGT 153
Db 496 AAGTTAGTAGTTTCTATGAATACTTTCGCGTGAATTTCAACCGATATAAGGATTA 555
QY 154 GAATTTAAATTTGCAAACTAGTAGTCAGATCAATAATAATTTTACGTGGA 201
Db 556 GTCAAAATATTGGTTAAACATTTTAAACGAAATTAATATGATTTTACATGCA 603

RESULT 13
US-09-621-976-17619
; Sequence 17619, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17619
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17619

Query Match      15.2%; Score 32.6; DB 4; Length 277;
Best Local Similarity 54.6%; Pred. No. 1.6;
Matches 65; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 96 GTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTCCCAAAGGACTTTTACTATGTGA 155
Db 157 GTAATTGCAATATCTTTAGGAGACCAAGGCGAGGAGTTCGGTTAATGTACACTGTTGAG 216
QY 156 ATTAATTTGTCAAACTAGTAGTCAGATCAATAATAATTTTACGTGGAAGAAAAA 214
Db 217 TTTTCGTACATATAAAATAATTGAAATAATACAAATTTTCTTCAAAAAA 275

RESULT 14
US-09-270-767-28358/c
; Sequence 28358, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28358
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28358

Query Match      15.2%; Score 32.6; DB 4; Length 495;
Best Local Similarity 63.3%; Pred. No. 2;
Matches 50; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 136 CAAAGGACTTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAATAATTTTA 195
Db 181 CAAATAAATTACATTAGAAATAATTTGTTTGTACCCCTACAAACAAAAATACAA 122
QY 196 CGTGGAAAAA 214
Db 121 AAATGAAAAA 103

RESULT 15
US-09-270-767-12569/c
; Sequence 12569, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12569
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12569
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:48 ; Search time 251.043 Seconds
(without alignments)
4898.046 Million cell updates/sec

Title: US-09-437-450A-34

Perfect score: 214

Sequence: 1 aaatctgctggcggtgca.....acgtgaaaaa 214

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	40.4	18.9	678	9	Sequence 358, App
C 2	38.2	17.9	60940	16	Sequence 88, Appl
C 3	38	17.8	3095	18	Sequence 312, App
C 4	37.8	17.7	2116	9	Sequence 31, Appl
C 5	37.8	17.7	2116	14	Sequence 15560, A
C 6	37.2	17.4	2782	18	Sequence 17285, A
C 7	36.2	16.9	1344	16	Sequence 70, Appl
C 8	35.8	16.7	5001	15	Sequence 74, Appl
C 9	35.8	16.7	5001	15	Sequence 34, Appl
C 10	35.8	16.7	5001	17	Sequence 13, Appl
C 11	35.8	16.7	5001	18	Sequence 70, Appl
C 12	35	16.4	745	9	Sequence 13, Appl

C 13	35	16.4	745	14	US-10-072-349-13	Sequence 13, Appl
C 14	35	16.4	2820	15	US-10-301-822-188	Sequence 188, App
C 15	35	16.4	2820	15	US-10-298-027-63	Sequence 63, Appl
C 16	35	16.4	2820	15	US-10-295-027-960	Sequence 260, App
C 17	35	16.4	2820	18	US-10-473-974-204	Sequence 204, App
C 18	35	16.4	2839	9	US-09-909-775-1	Sequence 1, Appl
C 19	35	16.4	2840	10	US-09-918-6248-59	Sequence 59, Appl
C 20	35	16.4	2840	15	US-10-264-820-26	Sequence 26, Appl
C 21	35	16.4	2840	15	US-10-093-322-23	Sequence 23, Appl
C 22	35	16.4	2840	16	US-10-044-564-23	Sequence 23, Appl
C 23	35	16.4	2840	16	US-10-240-425-374	Sequence 374, App
C 24	35	16.4	2840	17	US-10-450-826-140	Sequence 140, App
C 25	35	16.4	2840	18	US-10-723-860-1559	Sequence 1559, App
C 26	35	16.4	3000	18	US-10-723-860-5982	Sequence 5982, App
C 27	34.8	16.3	6593	15	US-10-311-455-451	Sequence 451, App
C 28	34.6	16.2	83391	17	US-10-433-793-134	Sequence 124, App
C 29	34.4	16.1	456	16	US-10-424-599-6847	Sequence 6847, App
C 30	34.2	16.0	186	18	US-10-357-930-19457	Sequence 19457, A
C 31	34.2	16.0	199	18	US-10-357-930-55273	Sequence 55273, A
C 32	34.2	16.0	756	10	US-09-814-353-6226	Sequence 6226, App
C 33	34.2	16.0	756	10	US-09-814-353-12504	Sequence 12504, A
C 34	34.2	16.0	367378	15	US-10-312-841-2	Sequence 2, Appl
C 35	34	15.9	544	13	US-10-027-632-63376	Sequence 63376, A
C 36	34	15.9	544	13	US-10-027-632-63377	Sequence 63377, A
C 37	34	15.9	544	13	US-10-027-632-63378	Sequence 63378, A
C 38	34	15.9	544	15	US-10-027-632-63376	Sequence 63376, A
C 39	34	15.9	544	15	US-10-027-632-63377	Sequence 63377, A
C 40	34	15.9	544	15	US-10-027-632-63378	Sequence 63378, A
C 41	34	15.9	582	9	US-09-731-872-94	Sequence 94, Appl
C 42	34	15.9	582	10	US-09-876-997-94	Sequence 94, Appl
C 43	34	15.9	634	13	US-10-027-632-37987	Sequence 37987, A
C 44	34	15.9	634	13	US-10-027-632-37988	Sequence 37988, A
C 45	34	15.9	634	13	US-10-027-632-37989	Sequence 37989, A

ALIGNMENTS

RESULT 1
US-09-770-149-358/c
; Sequence 358, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, MaJa
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 358
; LENGTH: 678

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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-358

Query Match
Best Local Similarity 18.9%; Score 40.4; DB 9; Length 678;
Matches 68; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 101 TGGAGTACTGTGAAGAGTTGCTCATGAAGTTTCCCAAGGACTTTTACTATGTGAATTAA 160
Db 120 TAGATTAAAGAGAACTATGGGAATTAAGTTTGAATATGTTTATGTTGTTGA 61

QY 161 ATTGTCAAACCTAGTAGTCAGATCAATAAAATTTTACGTGGAAATTAATTAATTAATTA 214
Db 60 GTTGTAACTTGTGTTTGCATAATAAATCGTTTGTAGTTTAAATTAATTAATTAATTA 7

RESULT 2
US-10-052-482-88
; Sequence 88, Application US/10052482
; Publication No. US20040072264A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 60940
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5047)..(7943)
; OTHER INFORMATION: "n" at positions 5047 to 7943 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (35382)..(35843)
; OTHER INFORMATION: "n" at positions 35382 to 35843 can be any base
US-10-052-482-88

Query Match
Best Local Similarity 17.9%; Score 38.2; DB 16; Length 60940;
Matches 70; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 89 TCCCAAGTTATTGGAGTACTGTGAAGAGTTGCTCATGAAGTTTCCCAAGGACTTTAC 148
Db 53600 TCACAAGAAATCATAGAAATTCATTAATAAAGAGTAAATTTTCTTAAATAT 53659

QY 149 TAGTGTGAATTAATTTGTCATCAATAGTAGTCAGATCAATAAAATTTTACGTGGAAATTA 208
Db 53660 AAATTAATAATTAATTTTAAATCAATAGCAATATAGAACTTACCAGGGAGAAAGAA 53719

QY 209 AAA 211
Db 53720 AAA 53722

RESULT 3
US-10-602-494-312/c
; Sequence 312, Application US/10602494
; Publication No. US20040265833A1
; GENERAL INFORMATION:
; APPLICANT: Cathy Lofton-Day
; APPLICANT: Andrew Sledziewski
; APPLICANT: Jeff Thomas
```

```
; APPLICANT: Robert W. Day
; APPLICANT: Lori Tonnes-Priddy
; APPLICANT: Karen Cardon
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
; FILE REFERENCE: 47675-45
; CURRENT APPLICATION NUMBER: US/10/602,494
; CURRENT FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 385
; SEQ ID NO 312
; LENGTH: 3095
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-602-494-312

Query Match
Best Local Similarity 17.8%; Score 38; DB 18; Length 3095;
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 113 AAGAGTTTCGTCTCATGAAGTTTCCCAAGGACTTTTACTATGTGAATTAATTTGTCAAACTA 172
Db 230 AAATCTTTTATAATAATTTTACAAAATAAATTTACAAAATTAATTAATTTTACAACTTA 171

QY 173 GTAGTCAGATCAATAAAATTTTACGTGGAAATTAATTAATTAATTAATTAATTAATTA 214
Db 170 TAACTCTCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 129

RESULT 4
US-09-925-297-261
; Sequence 261, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 261
; LENGTH: 2116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (35)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-261

Query Match
Best Local Similarity 17.7%; Score 37.8; DB 9; Length 2116;
Matches 81; Conservative 1; Mismatches 73; Indels 0; Gaps 0;

QY 60 ACATTTCCGATGTTCTCGAAAAGGACTTCCCAAGTATTGCGAGTACTGTGAAAGAGT 119
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Db 1841 AGAATGTGAGCGGCTTTCAGAGACAGCTCCATAAACTGTCTGGAGGCTGGGAAAAAAT 1900
Qy 120 TCCTCATGAAGTTTCCCAAGAGACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCA 179
Db 1901 TTGTCATGCATGCTTAATATGTAAGACACTCTTTAGTAATAATCGAAATTTGGTGATGGTA 1960

Qy 180 GATCAATAAAATTTTCAGTGGAAAAA 214
Db 1961 AAAAAAAAAATTTAAAAA 1995

RESULT 5

US-10-023-896-31
; Sequence 31, Application US/10023896
; Publication No. US20030027776A1
; GENERAL INFORMATION:
; APPLICANT: Victor Roschke
; TITLE OF INVENTION: 29 Human Cancer Associated Proteins
; FILE REFERENCE: PA004P1
; CURRENT APPLICATION NUMBER: US/10/023,896
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: unassigned
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US00/23794
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152,296
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/158,003
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (35)..(35)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-023-896-31

Query Match 17.7%; Score 37.8; DB 14; Length 2116;
Best Local Similarity 52.3%; Pred. No. 3.4;
Matches 81; Conservative 1; Mismatches 73; Indels 0; Gaps 0;
Qy 60 ACACATTCGATGTTCTCCAAAGAGCTTCCAAAGTATTGGAGTACTGTGAAGAGT 119
Db 1841 AGAATGTGAGCGGCTTTCAGAGACAGCTCCATAAACTGTCTGGAGGCTGGGAAAAAAT 1900
Qy 120 TCCTCATGAAGTTTCCCAAGAGACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCA 179
Db 1901 TTGTCATGCATGCTTAATATGTAAGACACTCTTTAGTAATAATCGAAATTTGGTGATGGTA 1960
Qy 180 GATCAATAAAATTTTCAGTGGAAAAA 214
Db 1961 AAAAAAAAAATTTAAAAA 1995

RESULT 6

US-10-425-115-15560/c

; Sequence 15560, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 15560
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_114191C.1
US-10-425-115-15560

Query Match 17.4%; Score 37.2; DB 18; Length 2782;
Best Local Similarity 56.6%; Pred. No. 5.5;
Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
Qy 93 AAAGTTATTGGAGTACTGTGAAAGAGTTCGTCAATGAAGTTTCCAAAGGACTTTTACTATG 152
Db 408 ACACATTTTGGCGTACTGTATTGTTTCTCTGTGTGTCAGCAATAGATTTTTCATTC 349
Qy 153 TGAATTAATTTGCAAACTAGTAGTCAGATCAATAAATTTTACGTGGAAAAA 212
Db 348 TAAATTAAGTGAATGTTTACTTGTGAATATATATGTTTGTGAATGCAAAAAA 289
Qy 213 AA 214
Db 288 AA 287

RESULT 7

US-10-282-122A-17285
; Sequence 17285, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Onisen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

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; PRIORITY APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17285
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Clostridium difficile
US-10-282-122A-17285

Query Match      16.9%; Score 36.2; DB 16; Length 1344;
Best Local Similarity 60.8%; Pred. No. 7.9;
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 115 AGAGTTGCTCATGAAGTTTCCCAAGGACCTTACTATGTGAATTAATTTGTCAAACTAGT 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 894 AAAGATTGCAAGAGATTTTGAAAGACCTTAAGTATGATATTAATTAATAAGT 953

QY 175 AGTCAGATCAATAAATTTTACGTGGAAAAA 211
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 954 TTTAATTAATAACAATATCATCATGATTATAGATAGAA 990

RESULT 8
US-10-172-086-70
; Sequence 70, Application US/10172086
; Publication No. US20030113750A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the differentiation
; FILE REFERENCE: of prostate tumors
; CURRENT APPLICATION NUMBER: US/10/172,086
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 70
; LENGTH: 5001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-172-086-70

Query Match      16.7%; Score 35.8; DB 15; Length 5001;
Best Local Similarity 49.7%; Pred. No. 17;
Matches 91; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 20 AACAGTCTTCTCAATTGGCAACTGCTATATCATCTCCGCAACACATTCGGATGTTCTCG 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1756 AAAAGTAGTTTGAATAATGTTAGATAGAGATTTTGAAAAATAATTTTGAAGTTTTTA 1815

QY 80 AAAGGACTTCCCAAGTTTGGAGTACTGTGAAGAGTTGCTCATGAAGTTTCCCAA 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1816 AAAAGGTTAGCGAAATGAAAGAAAAAATGGGAGATGGAATTAATTAATGAATGAG 1875

QY 140 GGACTTTTACTATGTGAATTAATTAATTTGCAAACTAGTAGTCAGATCAATAAATTTTACGTG 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1876 TGAATTTAGATTGGATTTTGAATTTTAAATAAGTATATATAAATAAATAGTTTTTAAAG 1935

QY 200 GAA 202
    ||
Db 1936 AAA 1938

RESULT 9
US-10-240-452-74
; Sequence 74, Application US/10240452
; Publication No. US20030162194A1
```

```
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Apoptosis
; FILE REFERENCE: 5013.1006
; CURRENT APPLICATION NUMBER: US/10/240,452
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03969
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 74
; LENGTH: 5001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-452-74

Query Match      16.7%; Score 35.8; DB 15; Length 5001;
Best Local Similarity 49.7%; Pred. No. 17;
Matches 91; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 20 AACAGTCTTCTCAATTGGCAACTGCTATATCATCTCCGCAACACATTCGGATGTTCTCG 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1756 AAAAGTAGTTTGAATAATGTTAGATAGAGATTTTGAAAAATAATTTTGAAGTTTTTA 1815

QY 80 AAAGGACTTCCCAAGTTTGGAGTACTGTGAAGAGTTGCTCATGAAGTTTCCCAA 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1816 AAAAGGTTAGCGAAATGAAAGAAAAAATGGGAGATGGAATTAATTAATGAATGAG 1875

QY 140 GGACTTTTACTATGTGAATTAATTAATTTGCAAACTAGTAGTCAGATCAATAAATTTTACGTG 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1876 TGAATTTAGATTGGATTTTGAATTTTAAATAAGTATATATAAATAAATAGTTTTTAAAG 1935

QY 200 GAA 202
    ||
Db 1936 AAA 1938

RESULT 10
US-10-311-507-34
; Sequence 34, Application US/10311507
; Publication No. US20040115630A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and nucleic acids for the analysis of astrocytomas
; FILE REFERENCE: 5013.1013
; CURRENT APPLICATION NUMBER: US/10/311,507
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07538
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 5001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
```

US-10-311-507-34

Query Match 16.7%; Score 35.8; DB 17; Length 5001;
Best Local Similarity 49.7%; Pred. No. 17;
Matches 91; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 20 AACAGTCTTCATTCGGAACCTGCTATATCATCTCCGCAACACATTTCCGATGTTCTCG 79
DB 1756 AAAAGTAGTTTGAAGATGTTAGAAATAGAGATTTTGAAGAAATAATTTTGAAGTTTGA 1815
QY 80 AAAAGGACTTCCCAAGCTTATTCGAGTACTGTGAAAGAGTTGCTCATGAAGTTTCCCAA 139
DB 1816 AAAAGGTACGGAATGAAGAGAAAAAATGCGAGATGTAATTAATGTAATGAG 1875
QY 140 GGAATTTACTATGTGAATTAATTTGTCAACTAGTCTAGATCAATATAAATTTTACGTG 199
DB 1876 TGATTTTAGATTGGATTTTGAATTTTAAATAAGTATATAAATAAATAAGTTTAAAG 1935
QY 200 GAA 202
DB 1936 AAA 1938

RESULT 11

US-10-480-846-70

; Sequence 70, Application US/10480846
; Publication No. US20040219549A1
; GENERAL INFORMATION:
; APPLICANT: Distler, Jurgen
; APPLICANT: Model, Fabian
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: Method and nucleic acids for the differentiation
; TITLE OF INVENTION: of prostate and renal carcinomas
; FILE REFERENCE: 47675-53
; CURRENT APPLICATION NUMBER: US/10/480,846
; PRIOR APPLICATION NUMBER: PCT/EP02/06603
; PRIOR FILING DATE: 2003-12-12
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: DE 10128509.4
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 70
; LENGTH: 5001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-480-846-70

Query Match 16.7%; Score 35.8; DB 18; Length 5001;
Best Local Similarity 49.7%; Pred. No. 17;
Matches 91; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 20 AACAGTCTTCATTCGGAACCTGCTATATCATCTCCGCAACACATTTCCGATGTTCTCG 79
DB 1756 AAAAGTAGTTTGAAGATGTTAGAAATAGAGATTTTGAAGAAATAATTTTGAAGTTTGA 1815
QY 80 AAAAGGACTTCCCAAGCTTATTCGAGTACTGTGAAAGAGTTGCTCATGAAGTTTCCCAA 139
DB 1816 AAAAGGTACGGAATGAAGAGAAAAAATGCGAGATGTAATTAATGTAATGAG 1875
QY 140 GGAATTTACTATGTGAATTAATTTGTCAACTAGTCTAGATCAATATAAATTTTACGTG 199
DB 1876 TGATTTTAGATTGGATTTTGAATTTTAAATAAGTATATAAATAAATAAGTTTAAAG 1935
QY 200 GAA 202
DB 1936 AAA 1938

RESULT 12

US-09-764-855-13/c

; Sequence 13, Application US/09764855

; Patent No. US20020119919A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior Application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (397)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (512)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (687)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (711)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-855-13

Query Match 16.4%; Score 35; DB 9; Length 745;
Best Local Similarity 64.9%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 138 AGGACTTTACTATGTGAATTAATTTGTCAACTAGTCTAGATCAATATAAATTTTACG 197
DB 98 AGGACATTTTATTTTAAATTTAAATTTTCAATCTAATGTTNANAAAAA 39
QY 198 TCGAAAAA 214
DB 38 AAAAAA 22

Query Match 16.4%; Score 35; DB 9; Length 745;
Best Local Similarity 64.9%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 138 AGGACTTTACTATGTGAATTAATTTGTCAACTAGTCTAGATCAATATAAATTTTACG 197
DB 98 AGGACATTTTATTTTAAATTTAAATTTTCAATCTAATGTTNANAAAAA 39
QY 198 TCGAAAAA 214
DB 38 AAAAAA 22

RESULT 13

US-10-072-349-13/c

; Sequence 13, Application US/10072349
; Publication No. US20030054420A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P110C1
; CURRENT APPLICATION NUMBER: US/10/072,349
; CURRENT FILING DATE: 2002-02-11
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 13
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature

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; LOCATION: (56)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (58)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (397)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (512)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (687)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (711)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-072-349-13

Query Match          16.4%; Score 35; DB 14; Length 745;
Best Local Similarity 64.3%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 138 AAGGACTTTACTATGTGAATTAATTTGTCAAAGTAGTAGTCAGATCAATAAAATTTTACG 197
Db 98 AGGACATTTTATTTAAATTAATTTACAATCTAATGGTNNAAAAAATTTTAAAAA 39

QY 198 TGGAAAAAATTTAAAAA 214
Db 38 AAAAAAATTTAAAAA 22

RESULT 14
US-10-301-822-188/c
; Sequence 188, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 2820
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)...(1278)
US-10-301-822-188

Query Match          15.4%; Score 35; DB 15; Length 2820;
Best Local Similarity 52.3%; Pred. No. 23;
Matches 103; Conservative 0; Mismatches 90; Indels 4; Gaps 1;

QY 17 TGCACACAGTCTTCTCAATTTGGCAACTGTCTATATCATTTCCGCAACACATTTCCGATGTTTC 76
Db 17 TGCACACAGTCTTCTCAATTTGGCAACTGTCTATATCATTTCCGCAACACATTTCCGATGTTTC 76

US-10-295-027-63/c
; Sequence 63, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziiz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 2820
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-295-027-63

Query Match          16.4%; Score 35; DB 15; Length 2820;
Best Local Similarity 52.3%; Pred. No. 23;
Matches 103; Conservative 0; Mismatches 90; Indels 4; Gaps 1;

QY 17 TGCACACAGTCTTCTCAATTTGGCAACTGTCTATATCATTTCCGCAACACATTTCCGATGTTTC 76
Db 17 TGCACACAGTCTTCTCAATTTGGCAACTGTCTATATCATTTCCGCAACACATTTCCGATGTTTC 76
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Qy	77	TCGAAAGGACTTCCCAAGTTATTGGAGTACTGTGAAAGAGTTCGTGATGAAGTTTCCC	136
Db	2337	TGATTAAAGTATCCCAACTGTCAGTAATCTCATTTTCAGAGGTGGAACCAACTTTCC-	2279
Qy	137	AAAGGACTTTACTATGTGAATTAAATTTGTCAAACTAGTAGTCAGATCAATAAAATTTTAC	196
Db	2278	---TCTCTGTACATTTATATTTAACTCCTCTCACATGTATTTAGGCAAGAAATATTTTA	2222
Qy	197	GTGGAATAAAAAAAAAA	213
Db	2221	AATGAGAGAAAAACAAA	2205

Search completed: January 22, 2005, 05:10:51
 Job time : 257.043 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:43 ; Search time 49.0695 Seconds
(without alignments)
3447.516 Million cell updates/sec

Title: US-09-437-450A-40
Perfect score: 238
Sequence: 1 ttttttttttttggaggga.....tacgtggcaaaaaaaaaa 238

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCUTUS_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	34	14.3	1605	4	US-09-248-796A-978
C 2	33.4	14.0	1208	3	US-09-461-474-11
C 3	32.8	13.8	459	4	US-09-270-767-9771
C 4	32.8	13.8	459	4	US-09-270-767-25053
C 5	32.4	13.6	495	4	US-09-270-767-28358
C 6	32.4	13.6	979	4	US-09-270-767-12569
C 7	32.4	13.6	1551	4	US-09-270-767-29950
C 8	32.4	13.6	1599	4	US-09-270-767-13884
C 9	32.4	13.6	1724	3	US-09-197-679A-1
C 10	31.8	13.4	832	4	US-09-621-976-2813
C 11	31.6	13.3	5183	2	US-08-870-518-7
C 12	31.4	13.2	6124	3	US-08-213-419B-3
C 13	31.4	13.2	29733	3	US-09-302-812-38
C 14	31.4	13.2	29793	3	US-09-511-477-38
C 15	31.4	13.2	29793	3	US-09-511-507-38
C 16	31.2	13.1	342	4	US-09-270-767-3861
C 17	31.2	13.1	342	4	US-09-270-767-19143
C 18	31.2	13.1	696	3	US-09-227-357-69
C 19	31	13.0	1410	4	US-08-248-796A-1405
C 20	30.8	12.9	2244	4	US-09-601-198-149
C 21	30.6	12.9	2410	4	US-09-710-279-4405
C 22	30.6	12.9	3378	4	US-09-710-279-3608
C 23	30.6	12.9	5761	4	US-09-799-451-23
C 24	30.6	12.9	1664976	4	US-08-916-421B-1
C 25	30.6	12.9	1664376	4	US-09-692-570-1
C 26	30.4	12.8	401	4	US-09-643-597-266
C 27	30.4	12.8	401	4	US-09-480-884A-266

ALIGNMENTS

RESULT 1

US-09-248-796A-978/c
; Sequence 978, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 978

; LENGTH: 1605

; TYPE: DNA

; ORGANISM: Candida albicans

US-09-248-796A-978

Query Match 14.3%; Score 34; DB 4; Length 1605;

Best Local Similarity 53.8%; Pred. No. 0.57;

Matches 70; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 75 ATTCCCAATCATCTTCGGATGTTCTCGAAAGGACTTCCCAAAGTATTGGAGTACTG 134

Db 1424 AATCTTAAACAAAATTCGCTAGATCTTGTAAGAAATCAAAAAATTTTCATCAATGTAT 1365

QY 135 TGAAGAGTTCGTCATGAAGTTTACCAAGGACTTTACTATGTGAATTAATTTGCAAA 194

Db 1364 CGATCATCTTCATATATAGATTTCAGAAAATTAATTAAGAAATCGGAAAAATTTTGAAA 1305

QY 195 CTAGTAGTCA 204

Db 1304 TTGTTGTCA 1295

RESULT 2

US-09-461-474-11/c

; Sequence 11, Application US/09461474

; Patent No. 6278042

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Rafalski, Antoni

; APPLICANT: Sakai, Hajime

; TITLE OF INVENTION: Plant Metal Transporters

; FILE REFERENCE: BB1303 US NA

; CURRENT APPLICATION NUMBER: US/09/461,474

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; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/112,562
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Glycine max
US-09-461-474-11

Query Match      14.0%; Score 33.4; DB 3; Length 1208;
Best Local Similarity 54.5%; Pred. No. 0.78;
Matches 67; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 52 CAATTGGCACTGCTCTATTATCAATCCGCAATCACATTTCGGATGTTCTCGAAGGAC 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 864 CAACAGCCCCCTTCAAGCTTAGTAGCATCTATCTCAGAGGTGTGTTCTCCATCAGGAC 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 112 TTCCCAAAAGTTATTGGAGTACTGTGAAAGAGTTTCGTCATGAAGTTTACCCAAAGGACTTT 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 804 TTCCAAATGTTTCGAGCATGTTGATGTTGTGCCCAATACAACTACTGAAAAGATTAG 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 172 ACT 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 744 AGT 742

RESULT 3
US-09-270-767-9771/c
; Sequence 9771, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9771
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-9771

Query Match      13.8%; Score 32.8; DB 4; Length 459;
Best Local Similarity 49.4%; Pred. No. 0.82;
Matches 85; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 23 TCACGGCGGGGATGCAACAGTCTTCTCTCAATTGGCACTGTCTATTATCCATTCCGCA 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 TAATGGCAGTTAAGCTTAAGATGTTTGCAAGTGTGTCATTAAATTATATGTTATCGT 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 83 ATCACATTTCCGATGTTCTCGAAAGAGCTTCCCAAGTTATTGGAGTACTGTGAAAGAG 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 CTATCAGTTATGATATGCTAAAAATGTAATGTTCATTTCATTGAGTTTAAGTTAAAAA 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 143 TTGCTATGAGTTTACCCAAAGGACTTTACTATGTAATTAATTTGTCAAA 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TTGTAAGCTTTTGGCCCTCTGCATGTGAAATGTATATTTACCGGCAAA 32
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-09-270-767-25053/c
; Sequence 25053, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
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; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25053
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-25053

Query Match      13.8%; Score 32.8; DB 4; Length 459;
Best Local Similarity 49.4%; Pred. No. 0.82;
Matches 85; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 23 TCACGGCGGGGATGCAACAGTCTTCTCTCAATTGGCACTGTCTATTATCCATTCCGCA 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 TAATGGCAGTTAAGCTTAAGATGTTTGCAAGTGTGTCATTAAATTATATGTTATCGT 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 83 ATCACATTTCCGATGTTCTCGAAAGAGCTTCCCAAGTTATTGGAGTACTGTGAAAGAG 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 CTATCAGTTATGATATGCTAAAAATGTAATGTTCATTTCATTGAGTTTAAGTTAAAAA 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 143 TTGCTATGAGTTTACCCAAAGGACTTTACTATGTAATTAATTTGTCAAA 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TTGTAAGCTTTTGGCCCTCTGCATGTGAAATGTATATTTACCGGCAAA 32
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-09-270-767-28358/c
; Sequence 28358, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28358
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28358

Query Match      13.6%; Score 32.4; DB 4; Length 495;
Best Local Similarity 62.2%; Pred. No. 1.1;
Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 157 TACCCAAAGGACTTTACTATGTAATTAATTTCTCAACTAGTAGCAGATCAATAAAT 216
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 TATGCAATAAATTTACATTTAGAAATAAATTTGTTGTTACCCCTACAAACAAAAAT 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 217 TCTACGTGCGCAAAAAA 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 ACNAAATGAAAAA 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-09-270-767-12569/c
; Sequence 12569, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12569
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12569
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Qy 217 TCTACGTGGCAAAAAA 238

; SOFTWARE: 28

NAME: FACELL, PIII
NO 2813


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Qy 214 AATTCTACGTGGCAAAAAAAAAAAAA 238
Db 21068 TTTTAATTTTTTGAAAAAAGAGAA 21044

RESULT 15
US-09-511-507-38/c
; Sequence 38, Application US/09511507
; Patent No. 6395543
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AME, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/511,507
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/302,812
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-511-507-38

Query Match 13.2%; Score 31.4;
Best Local Similarity 51.0%; Pred. No. 1
Matches 74; Conservative 0; Mismatch

Qy 94 GATGTCTCGAAAGGAGCTTCCCAAGTATTA
Db 21188 GATTTTCTACATCTCTATTGGCAACGATGTT

Qy 154 GTTTTACCCAAAGGACTTTTACTATGTCAATTTA
Db 21128 TTTTTCCTAATAAGTGAGATTCAAAATATTTT

Qy 214 AATTCTACGTGGCAAAAAAAAAAAAA 238
Db 21068 TTTTAATTTTTTGAAAAAAGAGAA 21044

Search completed: January 22, 2005, 02:14:46
Job time : 54.0695 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:48 ; Search time 279.197 Seconds
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Perfect score: 238
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Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	15.5	263	16	US-10-242-535A-49714 Sequence 49714, A
2	37	15.5	263	16	US-10-085-783A-49714 Sequence 49714, A
3	36.2	15.2	4233	16	US-10-041-018-135 Sequence 135, App
C 4	35.8	15.0	1510	18	US-10-739-930-3393 Sequence 3393, App
C 5	35.6	15.0	330926	18	US-10-719-993-7048 Sequence 7048, App
6	34.6	14.5	199	18	US-10-357-930-55273 Sequence 55273, A
7	34.2	14.4	308	16	US-10-424-599-87084 Sequence 87084, A
C 8	34.2	14.4	614	13	US-10-027-632-94282 Sequence 94282, A
C 9	34.2	14.4	614	13	US-10-027-632-305384 Sequence 305384, A
C 10	34.2	14.4	614	15	US-10-027-632-94282 Sequence 94282, A
C 11	34.2	14.4	614	15	US-10-027-632-305384 Sequence 305384, A
12	34.2	14.4	1560	18	US-10-739-930-3389 Sequence 3389, App

13	33.4	14.0	404	10	US-09-918-995-17073 Sequence 17073, A
C 14	33.4	14.0	499	9	US-09-783-590-5790 Sequence 5790, App
C 15	33.2	13.9	8781	15	US-10-311-455-1659 Sequence 1659, App
C 16	32.8	13.8	496	18	US-10-425-115-78614 Sequence 78614, A
C 17	32.8	13.8	678	9	US-09-770-149-358 Sequence 358, App
C 18	32.8	13.8	745	9	US-09-764-855-13 Sequence 13, Appl
C 19	32.8	13.8	745	14	US-10-072-349-13 Sequence 13, Appl
C 20	32.8	13.8	3423	16	US-10-398-221-3632 Sequence 3632, App
C 21	32.8	13.8	83391	17	US-10-433-793-124 Sequence 124, App
C 22	32.6	13.7	6117	15	US-10-240-485-43 Sequence 43, Appl
C 23	32.6	13.7	37184	17	US-10-433-793-107 Sequence 107, App
C 24	32.4	13.6	698	15	US-10-172-118-765 Sequence 765, App
C 25	32.4	13.6	698	16	US-10-342-887-765 Sequence 765, App
C 26	32.2	13.5	15373	15	US-10-311-455-440 Sequence 440, App
C 27	32.2	13.5	251364	14	US-10-175-523-58 Sequence 58, Appl
C 28	32.2	13.5	251364	14	US-10-175-523-61 Sequence 61, Appl
C 29	32.2	13.5	251364	14	US-10-175-523-79 Sequence 79, Appl
C 30	32	13.4	2133	14	US-10-074-475-86 Sequence 86, Appl
C 31	31.8	13.4	607	13	US-10-027-632-224261 Sequence 224261, A
C 32	31.8	13.4	607	15	US-10-027-632-224261 Sequence 224261, A
C 33	31.8	13.4	2000	9	US-09-938-842A-4562 Sequence 4562, App
C 34	31.8	13.4	2000	11	US-09-938-842A-4562 Sequence 4562, App
C 35	31.8	13.4	6565	16	US-10-221-714A-187 Sequence 187, App
C 36	31.8	13.4	96597	11	US-09-997-722-289 Sequence 289, App
C 37	31.8	13.4	402850	10	US-09-844-653-5 Sequence 5, Appl
C 38	31.6	13.3	506	17	US-10-021-323-5635 Sequence 5635, App
C 39	31.6	13.3	644	10	US-09-814-353-18833 Sequence 18833, A
C 40	31.6	13.3	778	15	US-10-106-698-589 Sequence 589, App
C 41	31.6	13.3	1873	14	US-10-175-523-37 Sequence 37, Appl
C 42	31.6	13.3	1873	18	US-10-723-860-6238 Sequence 6238, App
C 43	31.6	13.3	1887	17	US-10-437-963-45512 Sequence 45512, A
C 44	31.6	13.3	2034	11	US-09-973-278-872 Sequence 872, App
C 45	31.6	13.3	2787	11	US-09-973-278-873 Sequence 873, App

ALIGNMENTS

RESULT 1

US-10-242-535A-49714
; Sequence 49714, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49714
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-49714

Query Match 15.5%; Score 37; DB 16; Length 263;
Best Local Similarity 52.2%; Pred. No. 1;
Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 56 TGGCAACTGCTATTTCATTCGGAATCACATTCGATGTTCTCGAAAGACTTCC 115
Db 49 TGGTAAAGATTGATTAGTTACCTATTTTATCTAAATGGAGTTTAAAGATTG 108

QY 116 CAAAGTTATTGGAGTACTGTGAAGAGTTTCGTATGAGTTTACCCAAAGGACTTTACTA 175
DB 109 CTTTGCTTGATAGAAATTGTAACATCATGCTCCAGAGAAATATAATTCCAAATAATTACTA 168
QY 176 TGTGAATTAATTTCAAACTAGTACTAGTCAGATCAATA 212
DB 169 TAAAAAGTAAATTTTAAACTTTATGTTAAATTAACA 205

RESULT 2

US-10-085-783A-49714
; Sequence 49714, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49714
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-49714

Query Match 15.5%; Score 37; DB 16; Length 263;
Best Local Similarity 52.2%; Pred. No. 1;
Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 56 TGGCAACTGTCTATTATCCATCCGCAATCCACATTTCCGGATGTTCTCGAAAGGACTTCC 115
DB 49 TGTAAAGATTGATTATAGTACTCATTTTATCTTAATGAGTTTAAAGTTTG 108
QY 116 CAAAGTTATTGGAGTACTGTGAAGAGTTTCGTATGAGTTTACCCAAAGGACTTTACTA 175
DB 109 CTTTGCTTGATAGAAATTGTAACATCATGCTCCAGAGAAATATAATTCCAAATAATTACTA 168
QY 176 TGTGAATTAATTTCAAACTAGTACTAGTCAGATCAATA 212
DB 169 TAAAAAGTAAATTTTAAACTTTATGTTAAATTAACA 205

RESULT 3

US-10-041-018-135
; Sequence 135, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 4233
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
US-10-041-018-135

Query Match 15.2%; Score 36.2; DB 16; Length 4233;

Best Local Similarity 55.0%; Pred. No. 5.6;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 110 ACTTCCCAAGTTATTGGAGTACTGTGAAGAGTTTCGTATGAGTTTACCCAAAGGACT 169
DB 236 ACTTCTCAGTTTCATAAAGTATAGGATGGAATTCCTAAATTAACCTTTTAACTCAA 295
QY 170 TTAATAATGAAATTAATTTCAAACTAGTACTAGTCAGATCAATAAATTTCTACCTGCAAA 229
DB 296 TAAGTAAATGGATTAAATTTCCAGAAATTAATAACAGAAAAATTAATTTCAAAAGTATGA 355
QY 230 AAAAAAAA 238
DB 356 AATAAAAA 364

RESULT 4

US-10-739-930-3393/c
; Sequence 3393, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3393
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER2530_2
US-10-739-930-3393

Query Match 15.0%; Score 35.8; DB 18; Length 1510;
Best Local Similarity 65.7%; Pred. No. 4.8;
Matches 69; Conservative 0; Mismatches 32; Indels 4; Gaps 1;
QY 1 TTTTCTTTTTTTGGGAGGAATCACGGCGGC---GGATGCAACAGTCTTCTCTCAATT 56
DB 1395 TTTTCTTTTTTTGGGAGGAATTAAGGCGGCTCAGGAGCACTGCCATCTCCATTA 1336
QY 57 GGCAACTGTCTATTATCCATTCGCAATCACATTTTCGGATGTTCT 101
DB 1335 TCRAACTTTCCGTAGCAATTTATGCGAATACATTAGTAATGTTT 1291

RESULT 5

US-10-719-993-7048/c
; Sequence 7048, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7048
; LENGTH: 330926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(330926)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7)
US-10-719-993-7048

Query Match 15.0%; Score 35.6; DB 18; Length 330926;

Best Local Similarity 52.2%; Pred. No. 51;
Matches 56; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 149 ATGAAGTTTACCCAAAGGACTTTTACTATGTGAATTAAATTTGTCAAACTAGTAGTCAGATC 208
Db 32980 ATCATGTTTACTTAAACGTTTAAAGAGTAGAATTCAGTGTTCATCAATCAAGTACACACCTT 32921
QY 209 ATATAAATTTCTACGTGGCAAAAAA 238
Db 32920 AAAAAAATCAACATTCCTTTTAAAAA 32891

RESULT 6

US-10-357-930-55273
; Sequence 55273, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55273
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-55273

Query Match 14.5%; Score 34.6; DB 18; Length 199;
Best Local Similarity 61.8%; Pred. No. 4.7;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 150 TGAAGTTTACCCAAAGGACTTTTACTATGTGAATTAAATTTGTCAAACTAGTAGTCAGATCA 209
Db 57 TGCAGATACACAAATTGACACAAAAGGAAAAATAAAGTCAAACTGGTATTCAAAAA 116
QY 210 ATAAAAATTTCTACGTGGCAAAAAA 238
Db 117 AAAAAAATCAACATTCCTTTTAAAAA 145

RESULT 7

US-10-424-599-87084
; Sequence 87084, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 87084
; LENGTH: 308
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_49647C.1
US-10-424-599-87084

Query Match 14.4%; Score 34.2; DB 16; Length 308;
Best Local Similarity 60.0%; Pred. No. 7.3;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 144 TGTCTAGTGAAGTTTACCCAAAGGACTTTTACTATGTGAATTAAATTTGTCAAACTAGTAGTC 203
Db 57 TTGTGATATGGTTAAGAAAAATATATTACCATGTGCAGCACTATCTCTGAACATTGTT 116
QY 204 AGATCAATAAAATTTCTACGTGGCAAAAAA 238
Db 117 ATTACAAATTTATTTTCATGTGTCAAAAAA 151

RESULT 8

US-10-027-632-94282/c
; Sequence 94282, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94282
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-94282

Query Match 14.4%; Score 34.2; DB 13; Length 614;
Best Local Similarity 64.6%; Pred. No. 9.7;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 160 CCAAAGGACTTTACTATGTGAATTAAATTTGTCAAACTAGTAGTCAGATCAATTAATTC 219
Db 180 CCAATGTAGTCTCTAATTTAAATATAAGAAAGGAGGAGGAAGTAATAAAT 121
QY 220 ACGTGGCAAAAAA 238
Db 120 ATGTGACAAACAAAAACAGA 102

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RESULT 9
US-10-027-632-305384/c
; Sequence 305384, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305384
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-305384

Query Match      14.4%; Score 34.2; DB 13; Length 614;
Best Local Similarity 64.6%; Pred. No. 9.7;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 160 CCAAAGGACTTTACTATGTGAATTAATTTCTCAAACTAGTAGTCAGATCAATAAATTCCT 219
Db 180 CCCAATGTAGTCTCTAATGTTAATTAATAATAGAAAGGAGGACAGAGATATAATAAT 121

QY 220 ACGTGCAAAAAA 238
Db 120 ATGTGACACAAAAACAGA 102

RESULT 10
US-10-027-632-94282/c
; Sequence 94282, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305384
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-94282/c

Query Match      14.4%; Score 34.2; DB 15; Length 614;
Best Local Similarity 64.6%; Pred. No. 9.7;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 160 CCAAAGGACTTTACTATGTGAATTAATTTCTCAAACTAGTAGTCAGATCAATAAATTCCT 219
Db 180 CCCAATGTAGTCTCTAATGTTAATTAATAATAGAAAGGAGGACAGAGATATAATAAT 121

QY 220 ACGTGCAAAAAA 238
Db 120 ATGTGACACAAAAACAGA 102

RESULT 11
US-10-027-632-305384/c
; Sequence 305384, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305384
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-305384

Query Match      14.4%; Score 34.2; DB 15; Length 614;
Best Local Similarity 64.6%; Pred. No. 9.7;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 160 CCAAAGGACTTTACTATGTGAATTAATTTCTCAAACTAGTAGTCAGATCAATAAATTCCT 219
Db 180 CCCAATGTAGTCTCTAATGTTAATTAATAATAGAAAGGAGGACAGAGATATAATAAT 121

QY 220 ACGTGCAAAAAA 238
Db 120 ATGTGACACAAAAACAGA 102

RESULT 12
US-10-739-930-3389
; Sequence 3389, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
```

; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3389
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER246_1
US-10-739-930-3389

Query Match 14.4%; Score 34.2; DB 18; Length 1560;
Best Local Similarity 54.3%; Pred. No. 14;
Matches 69; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 112 TTCCCAAGTATTGGAGTACTGTGAAGAGTTTCGTCATGAAGTTTACCCAAAGGACTTT 171
DB 1260 TTCTCTCTTTTAAAGCACTAACTTAACTTATCTTATTTAGCTAGTAGCATCATCTGT 1319
QY 172 ACTATGCTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAAATTTCTACGTGGCAAAA 231
DB 1320 TTTATCTAAATTCGTTGGCGGATAAGTAGTAAGATTATACCAAGTGTTCACGTGCAAAA 1379
QY 232 AAAAAA 238
DB 1380 AAAAAA 1386

RESULT 13
US-09-918-995-17073
; Sequence 17073, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17073
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(404)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17073

Query Match 14.0%; Score 33.4; DB 10; Length 404;
Best Local Similarity 51.8%; Pred. No. 14;
Matches 100; Conservative 0; Mismatches 91; Indels 2; Gaps 1;
QY 46 TTCTCTCAATGGCAACTGCTATTATCCATCCGCAATCACATTTGGATGTTCTCGAA 105
DB 161 TTGTGTATATTGACAGAGCTCTTTTATACTAAAGCAAAATTTTAAATTTTGTACTAGAA 220
QY 106 AAGGACTTCCCAAGTTATTGGAGTACTGTGAAGAGTTTCGTCATGAAGTTTACCCAAAG 165
DB 221 AAAAAATTGAACATTTTAGTCTTGTGTTATAAAAAATGTTAAATTCAGAA--TTAGTTTAA 278
QY 166 GACTTTACTATGTGAATTAATTTGTCAAACTAGTAGTCAGATCAATAAATTTCTACGTGG 225
DB 279 GCCTTAATTAACATAATTAATAGCTTTGGACACTTAAAGAGCTCTAAATTTTCTGTGTA 338
QY 226 CAAAAA 238
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Db 339 AAAAAAAAAA 351
RESULT 14
US-09-783-590-5790/c
; Sequence 5790, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5790
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (127)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (211)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (233)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (362)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (270)
; OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature
LOCATION: (387)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (388)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (391)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (395)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (470)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (476)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (481)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (487)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (492)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (497)
OTHER INFORMATION: n equals a,t,g, or c

Query Match 14.0%; Score 33.4; DB 9; Length 499;

Best Local Similarity 50.3%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;

Matches 76; Conservative 0; TCGAATTCGGAGTTCGAAAGAGCTTCCCAAGTTATT 125

Db 281 CTACTAATAACNCCAAATNAAATTAATACTACTACTACAGAGCTTCCCACTTTTCA 222
Qy 126 GGAGTACTGTGAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAA 185
Db 221 TAAAGTTGTTANCAACATTTTGATTTTGGGTTATTTCAGAACATCTAACAGCAITGTTCTAA 162
Qy 186 ATTGTCAAACTAGTAGTCAGATCAATAAAAT 216
Db 161 AIGTTCAAAATTAAGGTAATTACATGAAT 131

RESULT 15

US-10-311-455-1659/c

Sequence 1659, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

PRIOR FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/EP01/07537

PRIOR FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 1659

LENGTH: 8781

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-311-455-1659

Query Match 13.9%; Score 33.2; DB 15; Length 8781;

Best Local Similarity 55.1%; Pred. No. 58;

Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 121 TTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180
Db 191 TTATATAATAACTTTATTACTATATAATAAATTAATAAATTAATAAATTAATAAATTAATAA 132
Qy 181 ATTAATTTGTCAAACTAGTAGTCAGATCAATAAAATTTACGTCGCAAAAAAATAA 238
Db 131 ATTATAATAACAATATATTAAACATATAAACAATAAATAAATAAATAAATAAATAAATAA 74

Search completed: January 22, 2005, 05:10:55

Job time : 283.197 secs

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:43 ; Search time 44.7398 Seconds
(without alignments)
3447.516 Million cell updates/sec

Title: US-09-437-450A-50

Perfect score: 217

Sequence: 1 tttttttttttttggagg.....gtcagatcaataaaattttc 217

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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3: /cgn2_6/ptodata/1/ina/6A-COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B-COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCUTS-COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	33.2	15.3	5855	1	US-08-592-214A-20
C 2	33.2	15.3	5855	3	US-09-149-976-20
C 3	31.2	14.4	4218	4	US-09-710-279-4205
C 4	31	14.3	516	4	US-09-270-767-8311
C 5	31	14.3	516	4	US-09-270-767-23593
C 6	31	14.3	1230025	4	US-09-198-452A-1
C 7	30.2	13.9	1001	4	US-09-671-317-1
C 8	30.2	13.9	1001	4	US-09-671-317-436
C 9	30.2	13.9	1113	4	US-10-081-644-1
C 10	30.2	13.9	49312	4	US-09-671-317-485
C 11	30	13.8	642	4	US-09-248-796A-6190
C 12	30	13.8	17056	3	US-09-245-041-3
C 13	30	13.8	17056	4	US-09-358-055B-3
C 14	30	13.8	17056	4	US-09-893-238-3
C 15	30	13.8	1830121	4	US-09-557-884-1
C 16	30	13.8	1830121	4	US-09-643-990A-1
C 17	30	13.8	1830121	4	US-10-329-960-1
C 18	29.6	13.6	10754	2	US-08-966-958-1
C 19	29.6	13.6	10754	2	US-09-215-817-1
C 20	29.6	13.6	10754	3	US-09-342-353-1
C 21	29.2	13.5	207	4	US-09-248-796A-11940
C 22	29.2	13.5	734	4	US-09-270-767-15119
C 23	29.2	13.5	1380	4	US-09-248-796A-3967
C 24	29.2	13.5	2634	2	US-08-907-166-7
C 25	29.2	13.5	2634	4	US-09-391-340-7
C 26	29.2	13.5	6583	4	US-10-204-708-26
C 27	29	13.4	31096	4	US-08-956-171E-59

Sequence 59, Appl
Sequence 4754, Ap
Sequence 11, Appl
Sequence 279, App
Sequence 3382, Ap
Sequence 19896, A
Sequence 142, App
Sequence 13, Appl
Sequence 12084, A
Sequence 3293, Ap
Sequence 454, App
Sequence 454, App
Sequence 23909, A
Sequence 3016, Ap
Sequence 3402, Ap
Sequence 3111, Ap
Sequence 11338, A
Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-592-214A-20/c
; Sequence 20, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin P.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5855 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5855
; OTHER INFORMATION: /note="sequence = Arabidopsis
; OTHER INFORMATION: thaliana CAL gene"
US-08-592-214A-20

Query Match 15.3%; Score 33.2; DB 1; Length 5855;
Best Local Similarity 48.2%; Pred. No. 0.99; Indels 0; Gaps 0;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 16 GGAGGAAATCAGCGCGCGGATCGAAGTCTTCTCAATTGGCAACTGTCTATATCAT 75
Db 1294 GAAGTACATATAGATGTTCTTGGTAGAGTTGAACCTTCAATTGACAACTGTGTTTGT 1235
QY 76 TCCGCAATCACATTTCCGATGTTCTCGAAAGGCATTCGAAAGTTATTGGAGTCATGTA 135
Db 1234 TGAGTCAATAGATTTCCAGCTTGGATATAAGATACAGCAGAGAAATTAATTTGAAGT 1175
QY 136 AAGAGTTCCGTCATGAGTTTACCCAAAGGCATTCATAGTGAATTAATTTGTCAACTAG 195
Db 1174 TTGGGTTAATNAAGGAAATATCCAAATACCAATTAAGTTTCTTTTGTACTAC 1115
QY 196 TAGTCAGATCA 206
Db 1114 TAAGCAATTA 1104

RESULT 2
US-09-149-976-20/c
; Sequence 20, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: YanoFSKY, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5855 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5855
; OTHER INFORMATION: /note= "sequence = Arabidopsis
; OTHER INFORMATION: thaliana CAL gene"
US-09-149-976-20

Query Match 15.3%; Score 33.2; DB 3; Length 5855;
Best Local Similarity 48.2%; Pred. No. 0.99;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 16 GGAGGAAATCAGCGCGCGGATCGAAGTCTTCTCAATTGGCAACTGTCTATATCAT 75
Db 1294 GAAGTACATATAGATGTTCTTGGTAGAGTTGAACCTTCAATTGCGCAACTGTCTATATCAT 1235

QY 76 TCCGCAATCACATTTCCGATGTTCTCGAAAGGCATTCGAAAGTTATTGGAGTCATGTA 135
Db 1234 TGAGTCAATAGATTTCCAGCTTGGATATAAGATACAGCAGAGAAATTAATTTGAAGT 1175
QY 136 AAGAGTTCCGTCATGAGTTTACCCAAAGGCATTCATAGTGAATTAATTTGTCAACTAG 195
Db 1174 TTGGGTTAATNAAGGAAATATCCAAATACCAATTAAGTTTCTTTTGTACTAC 1115
QY 196 TAGTCAGATCA 206
Db 1114 TAAGCAATTA 1104

RESULT 3
US-09-710-279-4205/c
; Sequence 4205, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4205
; LENGTH: 4218
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4205

Query Match 14.4%; Score 31.2; DB 4; Length 4218;
Best Local Similarity 50.0%; Pred. No. 3.7;
Matches 78; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 37 TCGAAGTCTTCTCTCAATTGGCAACTGTCTATATCATTCGCAATCACATTCGGATG 96
Db 3607 TCGAATTGAATTGGCGCAATAGCTGGCGTTGATATACGACTGACGCCCTTTAAAGA 3548
QY 97 TTCTCGAAAGGCATTCGAAAGTTATTGGAGTCATGTAAGAGTTTCGTCATCAAGTTTA 156
Db 3547 GCAATTAATCTATATTTCAAATTTAGTAGAATTAAGAGTTTAACATATCAATAAA 3488
QY 157 CCCAAAGGCATTCATAGTGAATTAATTTGTCAAAAC 192
Db 3487 AGAAATTCATAAAAGTTAAAGAAATATCAAAAC 3452

RESULT 4
US-09-270-767-8311
; Sequence 8311, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8311
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8311

Query Match 14.3%; Score 31; DB 4; Length 516;


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; NAME/KEY: primer_bind
; LOCATION: 45215..45233
; OTHER INFORMATION: 10-289-201.mis complement
; NAME/KEY: primer_bind
; LOCATION: 45722..45740
; OTHER INFORMATION: 10-290-37.mis
; NAME/KEY: primer_bind
; LOCATION: 45742..45760
; OTHER INFORMATION: 10-290-37.mis complement
; NAME/KEY: primer_bind
; LOCATION: 46010..46028
; OTHER INFORMATION: 10-290-326.mis
; NAME/KEY: primer_bind
; LOCATION: 46030..46048
; OTHER INFORMATION: 10-290-326.mis complement
; NAME/KEY: misc_binding
; LOCATION: 7552..7576
; OTHER INFORMATION: 10-286-289.probe
; NAME/KEY: misc_binding
; LOCATION: 7607..7631
; OTHER INFORMATION: 10-286-345.probe
; NAME/KEY: misc_binding
; LOCATION: 7637..7661
; OTHER INFORMATION: 10-286-375.probe
; NAME/KEY: misc_binding
; LOCATION: 17246..17270
; OTHER INFORMATION: 12-425-57.probe
; NAME/KEY: misc_binding
; LOCATION: 21583..21607
; OTHER INFORMATION: 12-421-140.probe
; NAME/KEY: misc_binding
; LOCATION: 36959..36983
; OTHER INFORMATION: 10-523-232.probe
; NAME/KEY: misc_binding
; LOCATION: 45202..45226
; OTHER INFORMATION: 10-289-201.probe
; NAME/KEY: misc_binding
; LOCATION: 45729..45753
; OTHER INFORMATION: 10-290-37.probe
; NAME/KEY: misc_binding
; LOCATION: 46017..46041
; OTHER INFORMATION: 10-290-326.probe
; OTHER INFORMATION: 10-290-326.probe
; US-09-671-317-485

Query Match      13.9%; Score 30.2; DB 4; Length 49312;
Best Local Similarity 58.2%; Pred. No. 20;
Matches 53; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 111 TTCAAAGTATTGGAGTCATGTGAAGAGTTGCTGATGAAGTTTACCCAAAGGCAATTC 170
Db 21185 TTCCAACTTATTAAATTTATCTGAGAAAGTAGAACAGGATGCTTCTCCAACTCATTTG 21126
QY 171 ATAGTGAATTAATTTGTCAACTAGTAGTCA 201
Db 21125 AACTAGGTCATCTGTATCAAAATGAGACA 21095

RESULT 11
US-09-248-796A-6190/c
; Sequence 6190, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208

; NAME/KEY: primer_bind
; LOCATION: 45215..45233
; OTHER INFORMATION: 10-289-201.mis complement
; NAME/KEY: primer_bind
; LOCATION: 45722..45740
; OTHER INFORMATION: 10-290-37.mis
; NAME/KEY: primer_bind
; LOCATION: 45742..45760
; OTHER INFORMATION: 10-290-37.mis complement
; NAME/KEY: primer_bind
; LOCATION: 46010..46028
; OTHER INFORMATION: 10-290-326.mis
; NAME/KEY: primer_bind
; LOCATION: 46030..46048
; OTHER INFORMATION: 10-290-326.mis complement
; NAME/KEY: misc_binding
; LOCATION: 7552..7576
; OTHER INFORMATION: 10-286-289.probe
; NAME/KEY: misc_binding
; LOCATION: 7607..7631
; OTHER INFORMATION: 10-286-345.probe
; NAME/KEY: misc_binding
; LOCATION: 7637..7661
; OTHER INFORMATION: 10-286-375.probe
; NAME/KEY: misc_binding
; LOCATION: 17246..17270
; OTHER INFORMATION: 12-425-57.probe
; NAME/KEY: misc_binding
; LOCATION: 21583..21607
; OTHER INFORMATION: 12-421-140.probe
; NAME/KEY: misc_binding
; LOCATION: 36959..36983
; OTHER INFORMATION: 10-523-232.probe
; NAME/KEY: misc_binding
; LOCATION: 45202..45226
; OTHER INFORMATION: 10-289-201.probe
; NAME/KEY: misc_binding
; LOCATION: 45729..45753
; OTHER INFORMATION: 10-290-37.probe
; NAME/KEY: misc_binding
; LOCATION: 46017..46041
; OTHER INFORMATION: 10-290-326.probe
; OTHER INFORMATION: 10-290-326.probe
; US-09-671-317-485

; SEQ ID NO 6190
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-6190

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Best Local Similarity 52.4%; Pred. No. 4.4;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 56 TTGGCAACTGTCATATCATTCGCGCAATCACATTCGGATGTTCTCGAAAAGGCATTCCA 115
Db 425 TTAGAACTTGCTGTTTACTTCATCATCACATTCGTTACCTACTAAATATCTGTGCA 366
QY 116 AAGTTATGGAGTCATGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGCATTTCATAGT 175
Db 365 TCCTCATTTGGCGTGTGAGTAAGTCTTGAACCAATTTTCAACATTTTCAAAATGATCTT 306
QY 176 GAATTA 181
Db 305 GAATCA 300

RESULT 12
US-09-245-041-3/c
; Sequence 3, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 17056
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-245-041-3

Query Match      13.8%; Score 30; DB 3; Length 17056;
Best Local Similarity 57.4%; Pred. No. 15;
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 TTTTITTTTTTTTTTGGGAGGAATCACGGCGGGGATCGAACAGTCTTCTCTCAATTGGC 60
Db 10097 TTATTTATTTTATTAAGAACTCAATAGTATGAGACATTTGTTAGACCTTAATTGAA 10038
QY 61 AACTGTCTATATCATTCGCGCAATCACATTTCCGA 94
Db 10037 AACTGTTCAAGTCAGTTCTCTTTTACATTTGGA 10004

RESULT 13
US-09-358-055B-3/c
; Sequence 3, Application US/09358055B
; Patent No. 6713277
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS INCLUDING
; TITLE OF INVENTION: OBESITY
; FILE REFERENCE: 7853-151
; CURRENT APPLICATION NUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
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; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 17056
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-358-055B-3

Query Match 13.8%; Score 30; DB 4; Length 17056;
Best Local Similarity 57.4%; Pred. No. 15;
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 TTTTNTTTTTTTGGGAGAAATCAGCGGGGGATCGAACAGTCTTCTCTCAATTGGC 60
DB 10097 TTATTTATTTATTTAAGAACTCAATAGTATGACATTTGTTAGCACCTAATTGAA 10038
QY 61 AACTGCTATATCATTCGCGCAATCACATTTCCGA 94
DB 10037 AACTGTTCCAGTCAGTCTCTTTTACATTGTGGA 10004

RESULT 14
US-09-893-238-3/c
; Sequence 3, Application US/09893238
; Patent No. 6727348
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; FILE REFERENCE: 7853-237
; CURRENT APPLICATION NUMBER: US/09/893,238
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/093,630
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/104,978
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 17056
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-893-238-3

Query Match 13.8%; Score 30; DB 4; Length 17056;
Best Local Similarity 57.4%; Pred. No. 15;
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 TTTTNTTTTTTTGGGAGAAATCAGCGGGGGATCGAACAGTCTTCTCTCAATTGGC 60
DB 10097 TTATTTATTTATTTAAGAACTCAATAGTATGACATTTGTTAGCACCTAATTGAA 10038
QY 61 AACTGCTATATCATTCGCGCAATCACATTTCCGA 94
DB 10037 AACTGTTCCAGTCAGTCTCTTTTACATTGTGGA 10004

RESULT 15
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 13.8%; Score 30; DB 4; Length 1830121;
Best Local Similarity 52.4%; Pred. No. 80;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 85 ACATTTCCGGATGTTCTCGAAAGGCAATTCCTGAGTCAATGTTGGAGTCAATGTTGAAAGAGTTTCG 144
DB 636437 ACAGCTTGATATCGCAAGCAGCGCAATCAATAATCGAAGGATTAGATTGATAGGCTTCC 636378
QY 145 TCATGAAGTTTACCCNAAGCAATTCATAGTGAATTAATTTGCAAACTAGTAGTCAGAT 204
DB 636377 TCAATAATTTTCAGGAGAGAAATAGCTGCAATAATAGGATTGGCTAATTTGTTAGCCAAT 636318
QY 205 CAATAA 210
DB 636317 AATAA 636312

Search completed: January 22, 2005, 02:14:56
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2005, 17:02:48 ; Search time 254.562 Seconds
(without alignments)
4898.046 Million cell updates/sec

Title: US-09-437-450A-50
Perfect score: 217
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Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	37	17.1	2159	16	US-10-425-114-7290
3	35.4	16.3	403035	17	US-10-741-601-5729
4	34.6	15.9	441	10	US-09-918-995-9159
5	34.2	15.8	1169	13	US-10-027-632-124305
6	34.2	15.8	1169	13	US-10-027-632-124306
7	34.2	15.8	1169	13	US-10-027-632-124305
8	34.2	15.8	1169	15	US-10-027-632-124306
9	34.2	15.8	3095	18	US-10-602-494-312
10	34	15.7	728	15	US-10-012-697-734
11	33.2	15.3	609	16	US-10-282-122A-18075
12	32.6	15.0	530	15	US-10-029-386-4708

C 13	32.4	14.9	1057	15	US-10-195-730-25	Sequence 25, Appl
C 14	32.4	14.9	1057	17	US-10-799-747-25	Sequence 25, Appl
C 15	32.4	14.9	3899	10	US-09-814-353-20529	Sequence 20529, A
16	32.2	14.8	17388	9	US-09-815-242-8512	Sequence 8512, Ap
17	32	14.7	811	13	US-10-027-632-155696	Sequence 155696,
18	32	14.7	811	13	US-10-027-632-155697	Sequence 155697,
19	32	14.7	811	15	US-10-027-632-155696	Sequence 155696,
20	32	14.7	811	15	US-10-027-632-155697	Sequence 155697,
21	32	14.7	871	15	US-10-012-697-1277	Sequence 1277, Ap
22	32	14.7	1458	16	US-10-424-599-59066	Sequence 59066, A
23	32	14.7	3771	16	US-10-282-132A-12168	Sequence 12168, A
C 24	31.8	14.7	2000	9	US-09-938-842A-4722	Sequence 4722, Ap
C 25	31.8	14.7	2000	11	US-09-938-842A-4722	Sequence 4722, Ap
26	31.8	14.7	2251	16	US-10-425-114-15082	Sequence 15082, A
27	31.8	14.7	2341	16	US-10-424-599-104234	Sequence 104234,
28	31.8	14.7	118951	14	US-10-161-572-11	Sequence 11, Appl
29	31.6	14.6	735	15	US-10-012-697-795	Sequence 795, App
30	31.6	14.6	736	15	US-10-012-697-673	Sequence 673, App
31	31.6	14.6	2000	9	US-09-938-842A-3182	Sequence 3182, Ap
32	31.6	14.6	2000	11	US-09-938-842A-3182	Sequence 3182, Ap
33	31.6	14.6	2004	9	US-09-887-576-200	Sequence 200, App
C 34	31.6	14.6	5875	15	US-10-311-455-261	Sequence 261, App
C 35	31.6	14.6	42123	13	US-10-087-193-1588	Sequence 1588, Ap
36	31.6	14.6	233528	18	US-10-719-993-6856	Sequence 6856, Ap
37	31.4	14.5	378	16	US-10-424-599-131794	Sequence 131794,
C 38	31.4	14.5	186510	15	US-10-043-715-1	Sequence 1, Appl
39	31.4	14.5	357652	17	US-10-322-696-34	Sequence 34, Appl
C 40	31.2	14.4	2327	15	US-10-101-510-410	Sequence 410, App
C 41	31	14.3	2000	9	US-09-887-576-85	Sequence 85, Appl
C 42	31	14.3	2004	9	US-09-887-576-218	Sequence 218, App
C 43	31	14.3	3095	18	US-10-602-494-1170	Sequence 170, App
C 44	31	14.3	15782	15	US-10-240-453-10	Sequence 10, Appl
45	31	14.3	127197	10	US-09-754-853A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-220-120-21/c
; Sequence 21, Application US/10220120
; Publication No. US20040048253A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Purvi
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Anissa L.
; APPLICANT: LIU, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKDREHER, Theresa K.
; APPLICANT: DAFFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.

APPLICANT: CHEN, Wensheng
APPLICANT: COHEN, Howard J.
APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT FILING DATE: 2002-08-26
PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
60/184,693; 60/184,771; 60/184,813; 60/184,773; 60/184,776;
60/184,769; 60/184,768; 60/184,837; 60/184,697; 60/184,841;
60/184,772; 60/185,213; 60/185,216; 60/204,863; 60/205,221;
60/204,815; 60/203,785; 60/204,821; 60/204,908; 60/204,226;
60/204,525; 60/205,285; 60/205,232; 60/205,323; 60/205,287;
60/205,324; 60/205,286
PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-05-17; 2000-05-12; 2000-05-16; 2000-05-15;
2000-05-16; 2000-05-17; 2000-05-17; 2000-05-17;
2000-05-17; 2000-05-17
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PERL Program
SEQ ID NO 21
LENGTH: 2950
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:034212.1:2000FEB01
FEATURE:
NAME/KEY: unsure
LOCATION: 52, 132
OTHER INFORMATION: a, t, c, g, or other
US-10-220-120-21

Query Match 18.4%; Score 40; DB 16; Length 2950;
Best Local Similarity 58.3%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 64 TGCTATATCATTCGCAATCACATTTCCGATGTTCTCGAAAGGCATTCCAAAGTTATT 123
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QY 124 GGAGTCATGTGAAGATTTCGTATGAAGTTTACCCAAAGGCATTCATATGTAATTA 183
Db 290 GAAGTCAGGCCACTGATTTCTTCAGGAAGTCTTTCCAACTGTTTCAGAGACATCTAA 231

RESULT 2
US-10-425-114-7290
Sequence 7290, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(531313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7290
LENGTH: 2159
TYPE: DNA
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: 700646607_FLI
US-10-425-114-7290

Query Match 17.1%; Score 37; DB 16; Length 2159;
Best Local Similarity 50.3%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 11 TTTTGGAGGAATCACGGCGCGGATCGAACAGCTCTTCTCAATTGGCAACTGTCTAT 70
Db 1828 TTTAGGAACAGTTCTCTGATGGCATATGAGGGGATTATTGACTCTCTACAACTGTACAT 1887

QY 71 ATCATTCCGCATACATTTCCGATGTTCTCGAAAGGCATTCCAAAGTTATTGGAGTCA 130
Db 1888 AACTACGGTTTCATCAGAAATGGAGGTTTACACGAGAGCGTCCCATATATAAAGGAGGC 1947

QY 131 TGTGAAGAGTTTCGTCGTAAGTTTACCCAAAGGCATTCATAGTGAATTAATTTGTCAA 190
Db 1948 TTCTAACATATACGTATAGTAGTGAAGCAAGGAATAAATAGTATATAAAAGAGAA 2007

QY 191 A 191
Db 2008 A 2008

RESULT 3
US-10-741-601-5729
Sequence 5729, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5729
LENGTH: 403035
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(403035)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-1;
US-10-741-601-5729

Query Match 16.3%; Score 35.4; DB 17; Length 403035;
Best Local Similarity 57.8%; Pred. No. 42; Indels 0; Gaps 0;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 103 AAAAGGCATTCCAAAGTTATTGGAGTCATGTGAAAGAGTTTCGTATGAAGTTTACCCAA 162
Db 51313 AAACCTCTTCTCAATGTTATTCATGTATACATAAGAGAGCATAGCTAAATATCCATG 51372

QY 163 GGCATTTTCATAGTAATTAATTTGTCAAACTAGTAGTCAGATCAATAAA 211
Db 51373 TGTTCCTCAAGTGAACACACTTGTGTAAACCACCACCTCAGATCAAGATA 51421

RESULT 4
US-09-918-995-9159
Sequence 9159, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hvsseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20


```

; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9159
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(441)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-9159

```

	Query Match	15.94;	Score 34.6;	DB 10;	Length 441;
	Best Local Similarity	52.4%;	Prod. No. 4.6;		
	Matches	76;	Conservative 0;	Mismatches 69;	Indels 0; Gaps 0;
Qy	64	TGCTATATCATTCGGCAATCACATTTCCGGATGTTCTCGAAAGGCATTCCAAAGTTATT	123		
Db	107	TATCTCTGAAATTCGTAAATTAAGTGAAGGAATTTCTATGAAAGTGCTTGGCAACCAATT	166		
Qy	124	GGAGTCATGTGAAAGAGTTTCGTATGAAGTTTACCCAAAGGCATTTTCATAGTGAATTTAAA	183		
Db	167	GGGCTATTATGATAGTTCTTAGTGGAAACATTATGTTTCTCCTCAATACACAGTGAATTGAG	226		
Qy	184	TTGTCAAACTAGTAGTCAGATCAAT	208		
Db	227	TTCTGACTCTCTGGGGCAGATAGAT	251		

```

RESULT 5
US-10-027-632-124305
; Sequence 124305, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124305
; LENGTH: 1169
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-124305
;
Query Match 15.8%; Score 34.2; DB 13; Length 1169;
Best Local Similarity 49.7%; Pred. No. 9;
Matches 84; Conservative 1; Mismatches 84; Indels 0; Gaps 0;
Qy 47 TTCTCTCAATTGGCAACTGTCATATCATTCGCAATCACATTCGCGATGTTCTCGAAA 106
Db 394 TTGAGTCTCTTASAAATCATTATCAGCCATTTTCCCCACATTTTGACTTCTATGAAATT 453
Qy 107 GGCATTCCAAGTTATTGGAGTCATGTGAAGAGTTGCTGTGAAGATTTCACCAAGGCA 166
Db 454 GGAATCTTAGATTCGAATGAATACTTTAAACAGTTTTCTGAAAGAAATAAAGAAACACCA 513

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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 124305
LENGTH: 1169
TYPE: DNA
ORGANISM: Human
US-10-027-632-124305

Query Match 15.8%; Score 34.2; DB 15; Length 1169;
Best Local Similarity 49.7%; Pred. No. 9;
Matches 84; Conservative 1; Mismatches 84; Indels 0; Gaps 0;
QY 47 TTCTCTCAATTGGCAACTGTCTATATCATTCGCAATCACATTCGATGTTCTCGAAA 106
DB 394 TTGAGTCTCTASAACTATATCAGCAATTTTCCCCCACTTTTGAATCTATGAAT 453
QY 107 GGCATTCCAAAGTTATGGAGTCATGTGAAGAGTTTCGTATGAAGTTTACCCAAAGGCA 166
DB 454 GGAATCTTAGATTCAATGAATACTTTAACAGTTTTTCTGAAGAATAAAAAAGAACACCA 513
QY 167 TTTCATAGTCAATTAATTTGTCAAACTAGTAGTCAGATCAATAAATTT 215
DB 514 CCCAATATGTACCTAAATTTTAAGATTATATTTAAATTTAAATTTAAATTT 562

RESULT 8

US-10-027-632-124306
Sequence 124306, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 124306
LENGTH: 1169
TYPE: DNA
ORGANISM: Human
US-10-027-632-124306

Query Match 15.8%; Score 34.2; DB 15; Length 1169;
Best Local Similarity 49.7%; Pred. No. 9;
Matches 84; Conservative 1; Mismatches 84; Indels 0; Gaps 0;
QY 47 TTCTCTCAATTGGCAACTGTCTATATCATTCGCAATCACATTCGATGTTCTCGAAA 106
DB 394 TTGAGTCTCTASAACTATATCAGCAATTTTCCCCCACTTTTGAATCTATGAAT 453

QY 107 GGCATTCCAAAGTTATGGAGTCATGTGAAGAGTTTCGTATGAAGTTTACCCAAAGGCA 166
DB 454 GGAATCTTAGATTCAATGAATACTTTAACAGTTTTTCTGAAGAATAAAAAAGAACACCA 513
QY 167 TTTCATAGTCAATTAATTTGTCAAACTAGTAGTCAGATCAATAAATTT 215
DB 514 CCCAATATGTACCTAAATTTTAAGATTATATTTAAATTTAAATTTAAATTT 562

RESULT 9

US-10-602-494-312/c
Sequence 312, Application US/10602494
Publication No. US20040265833A1
GENERAL INFORMATION:
APPLICANT: Cathy Lofton-Day
APPLICANT: Andrew Sledziewski
APPLICANT: Jeff Thomas
APPLICANT: Robert W. Day
APPLICANT: Lori Tonnes-Priddy
APPLICANT: Karen Cardon
TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
proliferative disorders
FILE REFERENCE: 47675-45
CURRENT APPLICATION NUMBER: US/10/602,494
CURRENT FILING DATE: 2003-06-23
NUMBER OF SEQ ID NOS: 385
SEQ ID NO 312
LENGTH: 3095
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-602-494-312

Query Match 15.8%; Score 34.2; DB 18; Length 3095;
Best Local Similarity 64.6%; Pred. No. 13;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 135 AAAGAGTTCGTATGAAGTTTACCCAAAGGCAATTCATAGTGAATTTAAATTTGCAAACTA 194
DB 230 AAAATCTTTATAATAATTTTACAAAATAAATTTACAAAATTAATTTAAATTTACACCTA 171
QY 195 GTAGTCAGATCAATAAAT 213
DB 170 TAACTCTCTCAAAAAAT 152

RESULT 10

US-10-012-697-734
Sequence 734, Application US/10012697
Publication No. US20030215803A1
GENERAL INFORMATION:
APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassam, Altaf
APPLICANT: Lamson, George
APPLICANT: Scott, Beth
APPLICANT: Drmanac, Radoje
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana
APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
ISOLATED FROM HUMAN PROSTATE
FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
CURRENT FILING DATE: 2003-01-21


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; OTHER INFORMATION: SWISSPROT HIT: P08547, EVALUE 1.00e-09
US-10-029-386-4708

Query Match      15.0%; Score 32.6; DB 15; Length 530;
Best Local Similarity 51.0%; Pred. No. 20;
Matches 77; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 39 GAACAGCTCTCTCAATGGCAACGTCATATATATTCGCGCAATCACATTTTCGGATGTT 98
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 GAAAAATTTCCCTTCTATTTCTTAGTTTGTAAATATATACGAGACATTTGGATTTT 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 99 CTCGAAAAGGCATTCCAAAGTTATTGGAGTCATGTGAAAAGAGTTCGTCAATGAAGTTTACC 158
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 GGCAAAATCTCTTCCACATTTATGAGATAATCAGGTGCTTTTGTCTGTGAACAAAGG 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 159 CAAAGGCATTTCTAGTGAATTAATGICA 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 ACAATTCATTGACACAGTAATTAATTATTTCA 216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-10-195-730-25/c
; Sequence 25, Application US/10195730
; Publication No. US20030144492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (348)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-195-730-25

Query Match      14.9%; Score 32.4; DB 15; Length 1057;
Best Local Similarity 56.6%; Pred. No. 30;
Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 60 CAACGTCTATATCATTCGCCAATCACATTTCCGATGTTCTCGAAAAGGCATTTCCAAAGT 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 CAAAATGCTGAACAGTCATCTTTTAGGTTCCTCAAGTGTCTTAAAGTGTTCCTCCAAAGT 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 120 TATTGGAGTCATGTGAAGAGTTGCTCATGAAGTTTACCCAAAGGC 165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 TTGAACAGGCATCAGATCACTTGGAGACATGTTTAAACAAAGAC 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-799-747-25/c
; Sequence 25, Application US/10799747
; Publication No. US20040157258A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/799,747
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/10/195,730
; PRIOR FILING DATE: 2002-07-16
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; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (348)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-799-747-25

Query Match      14.9%; Score 32.4; DB 17; Length 1057;
Best Local Similarity 56.6%; Pred. No. 30;
Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 60 CAACGTCTATATCATTCGCCAATCACATTTCCGATGTTCTCGAAAAGGCATTTCCAAAGT 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 CAAAATGCTGAACAGTCATCTTTTAGGTTCCTCAAGTGTCTTAAAGTGTTCCTCCAAAGT 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 120 TATTGGAGTCATGTGAAGAGTTGCTCATGAAGTTTACCCAAAGGC 165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 TTGAACAGGCATCAGATCACTTGGAGACATGTTTAAACAAAGAC 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-814-353-20529
; Sequence 20529, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20529
; LENGTH: 3899
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1_2_3, 3899
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-20529

Query Match      14.9%; Score 32.4; DB 10; Length 3899;
Best Local Similarity 56.6%; Pred. No. 50;
Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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Qy	60	CAACTGCTATATCATTCGCCAATCACATTCGGATGTTCTCGAAAAGGCATTCCAAAGT	119
Db	672	CAAAAATGCTGAACCCAGTCATCTTTTAGGTTCTCTCAAGTGTCTTAAAGTGTTCCTCCAAAGT	731
Qy	120	TATTGGAGTCATGTGAAAAGATTGTCATGAAGTTTACCCAAAGGC	165
Db	732	TTGAACAGGCATCAGATCATCTTGGAGACATGTTTAAACAAGAC	777

Search completed: January 22, 2005, 05:10:59
 Job time : 258.562 secs

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